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Title:
Perfect score:
Sequence:
                   1
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
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1: gb_bal:
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336
1 CGCTGCATCTTTTCTATGC.....CCCCNTTGGTTCCCAACCCA 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                    gb_in1:*
gb_in2:*
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em_htgo_inv:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

c 7	ന വ ക	ων	c 1	Result No.
41	59.2 59.2	78.8 73.8	80.6	Score
12.2 12.2	17.6 17.6	23.5	24.0	% Query Match
63739 115958	17.6 1769 17.6 1774	162409 1846	119945	% Query Match Length DB
77 85	944	93	92	DB
AC087621 AC004736	MMNDP	AC022184 HSNDPG	HSA218J18	ID
AC087621 Homo sapi AC004736 Human Chr	x83794 M.musculus X83397 M.musculus	ACUZZ184 Homo sapi X65882 H.sapiens m	AL034370 Human DNA	Description

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REFERENCE
AUTHORS
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ORGANISM
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KEYWORDS
                                                                                  COMMENT
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                                                                                                          JOURNAL
                                                                                                                    TITLE
                                                                                                                                                                                                CESSION
                                                                                                                                                                                                                                                                                                            requests: clonerequest@sanger.ac.uk
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                              HSA218J18 119945 bp DNA PRI 23-NOV-1999 HSA218J18 IN Sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete
                                                                                                 Submitted (26-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                             wray
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 119945)
                                                                                                                                                              Homo sapiens
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HTG; CCl.3 Splicing Factor; NDP; Norrie Disease; Pseudoglioma
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X89715 S.cerevisia
AL499624 Leishmani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            feature key.

IMPORPANT: This sequence is not the entire insert of clone 218J18.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MSTD repeat: matches 1. 9767. .9798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1840.
17665. .17883
/note-"L1M4 repeat: matches 4896. .5125 of consensus"
18105. .18239
/note-"L1M4 repeat: matches 7694. .7824 of consensus"
18357. .18532
                                                                                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 2605. 14577. .14986
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2447.
14071. .14210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MSTD 9797. .9923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Tigger3(Golem) repeat: matches 1. .3035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MLT1G repeat: matches 12. .155 of consensus" 11115. .11332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7888.
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/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                    /note="L1P repeat: matches 4891.
17144. 17247
                                                                                                                                                                                /note="AluSx repeat: matches 35.
16904. .16998
                                                                                                                                                                                                                                                                        16519.
                                                                                                                                                                                                                                                                                                                    15972
                                                                                                                                                                                                                                                                                                                               /note="MER74A repeat: matches 1..431 of consensus"
15386. 16018
/note="11MB4 repeat: matches 5181. .5827 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches
12651. .13006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12459
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11868. .12249
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/clone="RP6-218J18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1PA8 repeat: matches 555. .6155 of consensus"
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                                                                                                                                                                                                                                                                                          |5972. .16516
/note="L1P repeat:
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                                                                                                                 repeat: matches 2410.
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                                                                                                                                                                                                                                                                                            matches 4397. .4940 of consensus"
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                                                                                                                                                  /note="match: GSS 33571. .33727
                                                                                                                                                                                                    complement(33360.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MRKHVLAASFSMLSLLVIMGDTDSKTDSSFIMDSDPRRCMRHHY
VDSISHPLYKCSSKMVLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(30021. .30248,38694. .38867))
/gene="NDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(28998)
/gene="NDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/product="NDP" (Norrie Disease
complement(28998. .53726)
/gene="NDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: cDNAs X65724 X65882 X92397; match: ESTs
AA045724 AA670439 W61129 N59262 AA045724 AI129296 W61
N76731 R84741 H85821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="FLAM_A repeat: matches 1.
25646. .25750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="LIMC4 repeat: matches 7788. .7954 of consensus"
20579. .20700
   /note="MIR repeat: matches 27.
36253. .36416
                                                                             34667.
                                                                                                                 33816.
                                                                                                                                                                                                        /note="16 copies 2 mer ac
complement(33360. .33924)
                                                                                                                                                                                                                                                                                   33007
                                                                                                                                                                                                                                                                                                                        32205
                                                                                                                                                                                                                                                                                                                                                           31354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/product="NDP (Norrie Disease (Pseudoglioma))"
/protein_id="CaA22288.1"
/db_xref="GI:3947697"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(29013. .29019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L2 repeat: matches 2571. .2683 of consensus"
25901. .26177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="19 copies 2 mer tt 84% conserved"
25000. .25119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 17.
24827. .24928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 138.
22317. .22579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 9.
20970. .21069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 48.
20701. .20969
                                                                                                                                                                                                                                                                                                                    /note="AluJo repeat: matches 1. .308 of consensus"
32205. .32377
                                                                                                                                                                                                                                                                                                                                                                            /note="26 copies 2 mer aa 73% conserved"
                                                                                                                                                                                                                                                                                                                                                                                           /note="MER5B repeat: matches 58. .178 of consensus" 30652. .30703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="NDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"MIR repeat: matches 130. .238 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER33 repeat: matches 62.
23269. .23575
                                                       /note="L2 repeat: matches 2579. .2698 of consensus"
                                                                                                                               note-"MERSA repeat: matches 9.
                                                                                                                                                                                       /gene="NDP"
                                                                                                                                                                                                                                                            note="L2 repeat: matches
                                                                                                                                                                                                                                                                                                 note="FAM repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               LKALRLRCSGGMRLTATYRYILSCHCEECNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: proteins Q00604 P48744"
/codon_start=1
                                                                                          note="MIR repeat:
                                                                                                                                                                                                                                                                                   .33238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 24096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 copies 5 mer tttgt 85% .24998
                                                                         .34794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 25000
                                                                                                                                                                                                                                               .33381
                                                                                                                                                                     AQ042323"
                                                                                            matches
                                                                                                                                                                                                                                                              2177.
                                                                                                                                                                                                                           100%
                                                                                            7.
                                                                                                                                                                                                                                                                                                   .173
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                                                                                              . 213
                                                                                                                                                                                                                           conserved'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .262 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .138 of consensus"
                     .248 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .247 of consensus"
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                                                                                                                               .189 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .306 of consensus"
                                                                                                                                                                                                                                                              . 2417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .133 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .324 of consensus
                                                                                            of.
                                                                                                                                                                                                                                                                                                   of consensus"
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                                                                                            consensus"
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JOURNAL REFERENCE
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AUTHORS
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ORGANISM
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DEFINITION
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AC022184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
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                                                                                                                                                                                                                                                                                      TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38732 GATTCTATCAG--TCACCCATTGTACAAGTGTAGCTCAAAGGTAAGACCAAGGTCTCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
146; Conserv
                Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, C., Barna, N., Beckerly, R., Beda, F., Boukhyalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Honson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Forrest, G., Kann, L., Klein, J., Klein, J
                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Cai
1 (bases 1 to 162409)
Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 4 clone SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 4, clone RP11-52G4
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             upillun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56812. .57069
/note="MIR repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44406. .44483
/note="L1M4b repeat: matches 154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 41308. .41535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: STS AF020217" 51372. .51487
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40405. .40533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="31 copies 2 mer ag 90%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 2646. .2741 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162409 bp
  Lehoczky, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .48194
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Pred. No. 1.6e-15;
0; Mismatches 37;
  Levine, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               matches 5408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP11-52G4 map 4,
., Kann,L.,
., Lieu,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      рв 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .146 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 237
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  Liu,G.,
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                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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  Locke, K.,
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McPheeters,R.,

Meldrim,J.,

Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,

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FEATURES
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                                                                                                                                                  source
                                                                                                                                                                                                                                           36828 50972: contig of 14145 bp in length
50973 51072: gap of 100 bp
51073 68989: contig of 17917 bp in length
68990 69089: gap of 100 bp
69090 91875: contig of 2786 bp in length
91876 91975: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 188000; agarose-fp
Insert size: 161309; sum-of-contigs
Quality coverage: 3.7 in Q20 bases;
Quality coverage: 4.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 150398 bases at least 030 Consensus quality: 156259 bases at least 030 Consensus quality: 158583 bases at least 020 Consensus quality: 158583 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 52_G_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center
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20127 27970: contig of 7844 bp in length
27971 28070: gap of 100 bp
28071 36727: contig of 8657 bp in length
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6878 6877: gap of 100 bp
6878 8136: contig of 1259 bp in length
8137 8236: gap of 100 bp
8237 9996: contig of 1760 bp in length
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/clone="RP11-52G4"
                                                        /db_xref="taxon:9606"
/chromosome="4"
                                                                                                              organism="Homo sapiens"
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162409: cont:
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    Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,

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12552: contig of 2456 bp in length
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                                 Submitted (28-APR-1992) Z. Lab/Dept of Biochemistry, (2 (bases 1 to 1846)
                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1846)
                                                                                                                                                                                                 H.sapiens mRNA NDP
X65882 S61557
X65882.1 GI:35016
   Breakefield, X.O.,
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                               (bases 1 to 1846)
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8237 .9996
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Hendriks, R.W., Joblin d, X.O., Sims, K.B. and
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1. .6777
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Pred. No. 1.6e-15;
0; Mismatches 37;
              Jobling, M.A.,
                                            South Parks Road, Oxford OX1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108;
                                                                                                                                                                                                                             H.sapiens DNA for ORF1
           Berger, W.
Direct Submission
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteléostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1872)

Berger,W., Meindl,A., van de Pol,T.J., Cremers,F.P., Ropers,H.H.,

Doerner,C., Monaco,A., Bergen,A.A., Lebo,R., Warburg,M. et,al.

Isolation of a candidate gene for Norrie disease by positional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93265104
Submitted (08-APR-1992) W. Berger, University Hospital Nijmegen,
                                                                                       cloning
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                                                   Erratum:[[published
                                                                                                                                                                                                        chromosome.
                                       (bases 1 to 1872)
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                                                                           Genet. 1 (3), 199-203 (1992)
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VDSISHPLYKCSSKMVLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSK
LKALRLRCSGGMRLTATYRYILSCHCEECNS"
944 944 948
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85. .92
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/chromosome="Xpl1.23"
/dev_stage="fetal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:Q00604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA46713.1"
/db_xref="GI:35017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="retina"
/clone_lib="fetal retina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="NDP"
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and ORF2 from chromosome
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GACAGCTCGTNTCATGATCGACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107;
Submitted (05-JAN-1995) Z. Chen, Molecular Neurogenetics Lab, Massachusetts General Hospital-East, Building 149, 13th Stree Charlestown, MA 02129, USA Location/Qualifiers
                                                                        Chen, Z.
Direct Submission
                                                                                                                                                                                           Characterization and mapping of the
                                                                                                                                                                                                                   Chen, Z.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nijmegen,
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Nijmegen, THE NETHERLANDS
                                                                                                                                                                                                                                    Battinelli, E.M., Boyd, Y., Craig, I.W.,
                                                                                                                                                                                                                                                      Mammalia; Eutheria;
1 (bases 1 to 1769)
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                       NDP gene;
                                                                                                                                                                                                                                                                                                                                                                                                             M.musculus NDP gene.
                                                                                                                                     96432457
                                                                                                                                                                                                                                                                                                                                      house mouse.
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                                                                                                                                                                           ocus (Ndp)
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                                                                                                                                                       Genome 7
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/protein_id="CAA46640.1"
/db_xref="GI:1335017"
/translation="RHGGCDAGGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
/translation="RHGGCDAGGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
EAVRPARERLARKELROKRMQQFSRDSAYSSNKDSTCLLTERDTLGTSLQFPSPFSGT
ISFGSFSDSGIFPLGSQCCCLGFQQFSISGKKWALIHKRVRLSVFGARWGRIYFGK"
1 425 c 409 g 517 t
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417. .818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SWISS-PROT:000604"
/translation="MRKHVLAASFSMLSLLVIMGDTDSKTDSSFIMDSDPRRCMRHHY
VDSISHPLYKCSSKMVLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSK
                                                                                                                                                                                                                                                                                                                                                       GI:854318
Norrie disease locus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKALRLRCSGGMRLTATYRYILSCHCEECNS"
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/db_xref="GI:29947"
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/db_xref="taxon:9606"
/chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1769 bp
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Pred. No. 1.9e-14;
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BASE COUNT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (17-OCT-1995) W. Berger, MPI fuer Molekulare Genetik,
Ihnestrasse 73, D-14195 Berlin, FRG
                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus l bases 1 to 1774)

Berger, W., van de Pol, D., Bachner, D., Oerlemans, F., Winkens, H., Hameister, H., Wieringa, B., Hendriks, W., and Ropers, H.H.
                                                                                                                                                                                                                            Hum. Mol. Genet. 5 (1), 51-59 (1996) 96381426
                                                                                                                                                                                                                                                      mouse
                                                                                                                                                                                                                                                              An animal model for Norrie disease (ND):
                                                                                                                                                                                                                                                                                                                                                           house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                   X92397.1 GI:1177544
ND gene; Norrie disease locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                MMNORRIE 1774 by M. musculus mRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                              Berger,W.
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                                                                                                                                                                                                                                                  ND gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
           /tissue_type="brain"
1. .225
                                                        /db_xref="taxon:10090"
/chromosome="X"
                                          /dev_stage="19 weeks"
                                                                                      /strain="C57/b16"
'number=1
                                                                                                 /organism="Mus musculus"
                                                                                                                                ocation/Qualifiers
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//translation="mrnhyLAASISMLSLLAINGDTDSKTDSSFLMDSQRCMRHHYVD
SISHPLYKGSSKMYLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSKLK
ALRLRCSGGMRLTATYRYILSCHCEECSS"
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429. .8
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429. .824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA58725.1"
/db_xref="GI:854319"
/db_xref="MGD:MGI:102570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Norrie disease locus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="embryonic stem cells"
/cell_type="ES cells"
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/strain="L129"
/db_xref="taxon:10090"
/chromosome="X"
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87.7%;
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Norrie disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59.2; DB 94
Pred. No. 1.6e-08;
); Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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Best Local Similarity
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Birren, B., Linton, L., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campophano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Garo, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grizhugh, W., Gage, D., Galagan, J., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Murphy, T., Naylor, J., Nguyen, C., Nothu, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Naymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Sambok, L., Zimmer, A., and Zody, M., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GACAGCTCGTNTC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 63739)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-300E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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/gene="ND"
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/translation="MRNHVLAASISMLSLLAIMGDTDSKTDSSFLMDSQRCMRHHYVD
SISHPLYKCSSKMVLLARCEGHCSQASRSEPLYSFSTVLKQPFRSSCHCCRPQTSKLK
        Zimmer, A. and Zody, M.
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/protein_id="CAA63134.1"
/db_xref="GI:1177545"
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87.78;
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Pred. No. 1.6e-08;
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COMMENT
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This record contains 79 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           will be sequenced to completion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11683
Center clone name: 300_E_4
16881 16980; gap of 10
16981 17717; contig of 7
17918 17817; gap of 17
17918 18522; contig of 7
18523 18622; gap of 10
18623 19343; contig of 7
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801 1491: contig of 69
1492 1591: gap of 100 t
1592 2304: contig of 69
2304: contig of 7
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115 8114: gap of 100

115 8828: contig of 7:

129 8928: gap of 100

19 9622: contig of 60

19 3 9777:
                                                                                              15262: cor
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11230: c
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3926: cor
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16076: contig of
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13630: contig of
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ap of conti	46049: contig 46149: gap of 46864: contig 46964: gap of 47674: contig	9429: conti 9: gap of 5239: conti 9: gap of	4: gap or 3612: conti 2: gap of	42007: c 107: gap 42794: c	3: gap of 1221: conti 1: gap of	39598: co 698: gap o 40403: co	/: gap or 8800: conti 0: gap of	274: gap of 37987: conti	5: gap of 7174: cont	35513: conti 13: gap of 36345: conti	470	33905; c	33104	609: gap of 32297: conti	3:	9892: conti 2: gap of	29085: c	826 4	6775: gap of 27470: conti	26675: c	5151: gap of 25851: conti	4347: gap of 25051: conti	9: gap of 4247: conti	2737: gap of 23439: conti	1910: gap of 22637: conti		0261: gap of 20983: conti	20161: c
100 bp f 691 bp 100 bp f 706 bp	10 bp	dq 001 dq 001 dq 100 pp	100 bp	86 bp 0 bp 87 bp	100 bp 718 bp 100 bp	698 bp 00 bp 705 bp	713 bp	100 bp f 713 bp	100 bp f 729 bp	5 bp	703 bp	01 pp	07 bp	100 bp	dq 90 dq 0 dq 11	100 bp	21 bp	5 4 6	d dd s	24 bp	100 bp	0 bp	8	ÑĠ		7 6	N	of 718 bp
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AC004736/c
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      3 (bases 1 to 115958)
Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
Buettner,J., Bumeister,R., Card,P., deSailboat,F., Dunn,J.,
English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
Grant,O., Hahner,L., Harris,J., Lewis,E., Loo,H., Loo,K.N.,
                                                                                                                    Submitted (23-MAY-1998) Genome Science & Technology Center, University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd, Dallas, TX 75235-8591, USA
                                                                                                                                                                                                                            2 (bases 1 to 115958)
EVANS,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
Buettner,J., Bumeister,R., Card,P., deSailboat,C., Dunn,J.,
English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotwa
Grant,O., Hahner,L., Harris,J., Lewis,E., Loo,H., Loo,K.N.,
McFarland,J., Miller,R., Newton,J., Osborne-Lawrence,S.,
                                                                                                                                                                                                                                                                                                                                                                                             Evans, G.A., Athanasiou, M., Aguayo, P., Armstrong, D., Basit, M. Buettner, J., Bumeister, R., Card, P., deSailboat, F., Dunn, J., English, C., Ethridge, S., Garner, H.R., Gee, V., Gordon, M., Gol Grant, O., Hahner, L., Harris, J., Lewis, E., Loo, H., Loo, K.N., Major, T., McFarland, J., Newton, J., Osborne-Lawrence, S., Schageman, J., Schultz, R.A., Stimson, S., Syed, M. and Ward, T.
                                                                                                                                                                                                        Schageman, J., Schultz, R.A., Stimson, S., Syed, M. and Ward, T.
                                                                                                                                                                                                                                                                                                                                                                                           HTGS
                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 115958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC004736 115958 bp DNA PRI 03-JUL-1998 Human Chromosome 11p14.3 PAC clone pDJ1082L12 containing KNCN1 and MyOD, complete sequence.
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50840 50939: gap of 100 bp
50940 51664: contig of 725 bp in length
51665 51764: gap of 100 bp
51765 52477: contig of 713 bp in length
52478 52577: gap of 100 bp
52578 53281: contig of 704 bp in length
53382 53381: gap of 100 bp
54182 54181: gap of 100 bp
54182 54181: gap of 100 bp
54182 54877: contig of 666
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54877: contig of 696 bp
54977: gap of 100 bp
55682: contig of 705 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55782: gap of
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Pred. No. 0.019;
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of 647 bp
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Osborne-Lawrence, S.
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SOURCE

TITLE

/rpt\_f 60940.

family="L1"

rpt\_family="Alu"

/rpt\_family="THE1" 60398. .60596 complement(60013 59316

\_family="L1"

complement (58027

58249)

\_tamily="MER20"

/rpt\_tamily="MIR"

/rpt\_famil 57204. .57

y="MIR"

complement(41971. /rpt\_family="MIR" complement(39712.
/rpt\_family="MIR" complement (36023

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/rpt\_family="MIR" /rpt\_family="MIR"

/rpt\_family="Tigger1" complement(31777. .31

/rpt\_family="MIR" 28877. .31250

/rpt\_t 23678.

complement(21561. /rpt\_family="Alu" complement(19171 /rpt\_tamily="Alu"

4409

/rpt\_family="MIR"

.19291)

/organism="Homo sapiens" /db\_xref="taxon:9606"

.115958

VERSION

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MAPPED CLONE OVERLAP: pDJ59mi8 and 6-109h6.

IMPORTANT: This submission contains the entire insert of clone pDJ1082L12. pDJ1082L12 comes from a PAC library constructed atthe pDJ1082L12 comes from a PAC library constructed atthe clone has been finished according to strict quality criteria and attempts have been made to resolve all base calling problems such as compressions and repetitive elements. The expected Phred/Phrap calculated errors/10kb is 0.39. In addition, this sequence has been finished such that 99.9% of consensus base calls consist of either double-stranded coverage or 2 types of labeling chemistry c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Extent of pDJ1082L12 overlap with mapped clones; SP6 PAC cloning end: 1. 8775, pDJ59ml8; T7 PAC cloning end: 45252. .115958 6-109h6. Further information regarding the map of this region or annotation of pDJ1082L12 can be found at http://gestec.swmed.edu/chromoso2.htm. CHROMSOMAL LOCUS: This PAC clone comes from the Usher syndrome region (USH1C) mapped between STSs markers DJ1S1310 and 1115A14. MARKER CONFIRMATION: STSS/ESTS sequence confirmed; D11S4130, KNCN1,
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4 (bases 1 to 115958)

Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M. Buettner,J., Bumeister,R., Card,P., deSailboet,F., Dunn,J., English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gol Grant,O., Hahner,L., Harris,J., Lewis,E., Loo,H., Loo,K.N., Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S., Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and Ward,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-JUL-1998) Genome Science & Technology Center, University of Texas Southwestern Medical Center, 5323 Harry Blvd, Dallas, TX 75235-8891, USA On Jul 1, 1998 this sequence version replaced gi:3152625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and MyoD1
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Location/Qualifiers
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                                                                                                                                                                                                                                  233 TGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGCNCATGGCAGTCCTTGGN 292
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                                            ACO10136 171453 bp DNA HTG 22-MAR-20 HOMO Sapiens chromosome UNK clone RP11-129D2, WORKING DRAFT SEQUENCE, 2 unordered pieces.
                AC010136.7 GI:13431097
                                 AC010136
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HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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/rpt_family="MIR"
complement(90686.
/rpt_family="MIR"
91042. 91163
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86387
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complement(112629. .112992)
/rpt_family="L1"
29554 c 29450 g 28568 t
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/rpt_family="L1"
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complement(107302..107596)
/rpt_family="Alu"
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105586
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/rpt_family="L1"
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/rpt_family="MLT1"
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94274. .94419
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84727. .85172
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complement(82106.
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111412. .111792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(110473.
/rpt_family="Alu"
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105673. .105884
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/rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                       Score 41; DB 85; Length 115958; Pred. No. 0.019; 0; Mismatches 67; Indels 0;
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                                       202 CCCCGNNTGGCCCTGAGNTTCCAGAGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer ET; 52% of reads chemistry: Dye-terminator Big Dye; 48% of reads Assembly program: Phrap; version 0.990319 consensus quality: 169816 bases at least Q40 consensus quality: 170375 bases at least Q30 consensus quality: 170797 bases at least Q20 consensus quality: 170797 bases at least Q20 Insert size: 198000; agarose-fp Insert size: 171353; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Mar 22, 2001 this sequence version replaced gi:11990739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 171453)
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 7.08 in Q20 bases; agarose-fp Quality coverage: 7.13 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                        h 10.4%;
Similarity 52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                       38981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 32328: contig of 32328 bp in length
32329 32428: gap of unknown length
32429 171453: contig of 139025 bp in length
                                                                                     Conservative
                                                                                                                                                                                                                                                                                 vector_side:left"
32429 ..171453
/note="assembly_name:Contig8
                                                                                                                                                                                                                  vector_side:right"
41426 c 46891 g
                                                                                                                                                                                                                                                                clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig7
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="UNK"
/clone="RP11-129D2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- Genome Center -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 to 171453)
                                                                                                                                                                                                                                                                                                                                                                                                    .32328
                                                                                   Score 34.8; DB 61;
Pred. No. 2.2;
0; Mismatches 54;
                                                                                                                                                                                                                       44055 t
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                                                                                                                                                                                                                    100 others
                                                                                                                             Length 171453;
                                                                                       Indels
                                                                                     0;
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RESULT 1
AB033016
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RESULT 11
AC018471/c
                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
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                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                             2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                               2768 GACAGCTTGACAGCTGGTCAAGACGGTCAC 2797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 GNAAAGGGGCCCGCNCATGGCAGTCCTTGGNCAGNAGNAANGGANTTGGNCCCA 315
                                                                                                                     62 GACAGCTCGTNTCATGATCGACTCGGACCC 91
                                                                                                                                                                                GTTTCATGTTCTTGTACACTTCCCCTCTGGGATCAGGTGAGGGGTCCAGACAGCTGACCA 2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-OCT-1999) to the DDBJ/EMBL/GenBank databases. Osamu ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain DNA Res. 6 (5), 329-336 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohara, O., Nagase, T. and Kikuno, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SK plus clone:hg03443a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB033016.1 GI:6330337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB033016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirosawa, M., Nagase, T., Ishikawa, K., Kikuno, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20039618
                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                 693
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="KIAA1190"
<1. .527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="KIAA1190 protein"
/protein_id="BAA86504.1"
                                                                                                                                                                                                                                                                                                                                                                                    PTTASPGGRMNANN"
                                                                                                                                                                                                                                                                                                                                                                                                       KAHKEKCFRVSHTLAGDGVPAAPGLPPTQPQAHALPLLPGLPQTLPPPPHLPPPPPLF
                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="kpfrcencnerfqykyqlrshmsihighkqfmcqwcgkdfnmkq
yfdehmkThTgEkpyiceicGkSfTSRpnmkRhRrThTgEkpypcDvCgQrfrfsnmL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Start codon is not identified."
/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="hg03443a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA86504
/db_xref="GI:6330338"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="KIAA1190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3510
                                                                                                                                                                                                                                                              9.8%;
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for KIAA1190 protein,
                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                               1019 g
                                                                                                                                                                                                                                                            Score 33; DB 85; Length 3510; Pred. No. 7.5;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                 741 t
                                                                                                                                                                                                                                             36;
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REFERENCE
AUTHORS
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L.C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L.C., Kratovic,J., Kureshi,A., Landry,N., Lid,J., Liu,W.,
Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Martinez,E., Massey,E., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Morgan,M., Morris,S., Moser,M., Nelceod,M.P., Meador,N.,
Morgan,M., Morris,S., Moser,M., Nickerson,E., Newtson,N.,
Moyyen,A., Nguyen,N., Nickerson,E., Newtson,N.,
Nguyen,N., Nguyen,N., Nickerson,E., Newtson,N.,
Nguyen,N., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodeggren,E., Sonaike,T., Sparks,A., Stanley,H.,
Sutton,A., Svatek,A., Tabor, P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
Watlington,S., Walliams,G., Williamson,A., Wlaczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
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Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hannilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (12-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2000 this sequence version replaced gi:9719644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
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1 (bases 1 to 164036)
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Chemistry: Dye-primer Bodipy: 46% of reads Chemistry: Dye-terminator Big Dye: 54% of reads Assembly program: Phrap, version 0.990329 Consensus quality: 150896 bases at least Q40
                                                                                                                                                                                                                                              Center clone name: RP11-132K4
                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.ed
                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College
Center code: BCM
                                                                                                                                                             Sequencing vector: M13; L08821
                                                                                                                                                                                                                                                                                        Center project name: HMVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164036 bp
                                                                                                                                                                                                            --- Summary Statistics
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                                                                                                                                                                                                                                                                                                                              Project Information
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Jb 112240 GACAGCTTGACAGCTGGTCAAGACGGTCAC 112211
                                                                                                                                                                       BASE COUNT
ORIGIN
                                                   Db 112300 GTTTCATGTTCTTGTACACTTCCCCTCTGGGATCAGGTGAGGGGTCCAGACAGCTGACCA 112241
                                                                                                                                                                                                                                                                    SATURES
                                                                                                                     Query Match
Best Local
                                                                                                       Matches
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                          62
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                       GACAGCTCGTNTCATGATCGACTCGGACCC 91
                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                      43123
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                                                                                                                                                                                                           1. .164036
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
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                                                                                                                  9.8%;
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of 4337
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of 8607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FittHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPeneters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2000 this sequence version replaced g1:8778492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N. Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theo Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D.,
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Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,I
Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 15, clone RP11-296G21 Unpublished
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SEQUENCE, 22 unordered piece
ACO22064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choepel,Y.,
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Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 169523 bases at least 040
Consensus quality: 175394 bases at least 030
Consensus quality: 177188 bases at least 020
Insert size: 170000; agarose-fp
Insert size: 178259; sum-of-contigs
Quality coverage: 5.2 in 020 bases; sum-of-contig:
Quality coverage: 5.0 in 020 bases; sum-of-contig:
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
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1 1137: contig of 1137 bp in length
1138 1237: gap of 100 bp
1238 2271: contig of 1034 bp in length
2272 2371: gap of 100 bp
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Primates;
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RP11-296G21 map 15, WORKING DRAFT
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Wu,X., Wyman,D., Ye,W.J.,
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55506 71682; contig of 16177 bp in
71683 71782; gap of 100 bp
71783 97873; contig of 26091 bp in
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20900 25005: con
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17048 17147: gap of 100 bp
17148 18830: contig of 1683 bp in length
18831 18930: gap of 100 bp
18831 18930: gap of 100 bp
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6104 7238; contia of
7239 7230
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8890 .10365
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17148. .18830
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11752. .13621
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4932. .6003
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2372. .3377
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15744. .17047
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13722. .15643
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1238. .2271
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/db_xref="taxon:9606"
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10365: contig of 1476 bp
10465: gap of 100 bp
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3477: gap
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3184: contig of 6779 bp in length
384: gap of 100 bp
44283: contig of 12299 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55405: contig of 11022 bp in length
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15643: contig of 1922 l
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Simon,M.L., Vo,Q.K., Wei,Y., William
Naylor,S.L. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,J., Chen,Z., Culpepper,P., Ding,Y., Dugan,S.P., Durbin,K.J., Forcum,J., Ganesh,R.P., Garcia,C., Garcia,D.K., Gorrell,H., Gorrell,L.L., He,X., Hernandez,J., Jackson,L.E., Kondejewski,N., Leal,B., Lichtarge,O., Liu,W., Logan,O., Lu,J., Martinez,C., Moore,S., Moorish,T., Ngyuen,N., Oswal,G., Panpell,L.R., Parish,B.J., Derong, I. W., Deshid, N.D., Diroc, C. W., College, S., Charles, C., Parish,B.J., Derong, I. W., Deshid, N.D., Diroc, C. W., College, S., Charles, C., Parish,B.J., Derong, I. W., Deshid, N.D., Diroc, C. W., College, S., Charles, C., Parish,B.J., Derong, I. W., Deshid, N.D., Diroc, C. W., College, S., Charles, C., Parish,B.J., Derong, I. W., Deshid, N.D., Diroc, C. W., College, S., Charles, C., Parish, B.J., Derong, I. W., Deshid, N.D., Diroc, C. W., College, C., Charles, C., Parish, B.J., Derong, I. W., Deshid, N.D., Derong, C. W., College, C., Charles, C., Charles, C., Charles, C., Chen, Z., Charles, C., Chen, Z., Chen, Z
Submitted (30-MAR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                Worley, K.C.
Direct Submission
                                                                                                                                                          Submitted (26-NOV-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                    Direct Submission
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2 (bases 1
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Homo sapiens PAC RPCI4-613B23 (Roswell Park Cancer
PAC Library) complete sequence.
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25106. .31884
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97974. .127625
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clone_end:T7
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127726. .180359
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20900. .25005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .20799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
                                                                                                                                                                                                                                                                                                                                                                                                               Williamson, A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                                                                                                                                                           Pampell,L.R., Parish,B.J.,
.M., Scherer,S.E., Shen,H.,
liamson,A.L., Worley,K., Zhc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 180359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                   Position
28864
28865
32674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 30, 1999 this sequence version replaced gi:4263627.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                            53006
84131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rates than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
   100219
109068
109069
149456
149636
158518
163739
167565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Number of consensus changing Number of N's in consensus :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40 : Number of consensus changing edits:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contig length:
Phrap values in estimate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUALSTAT-REPORT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            local mapping efforts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baylor Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ytor Plaza, Houston, TX 77030, (bases 1 to 185161)
gagggcgggg(n)tgagacgaag
ttttgttcca(n)tnatctgtgt
                                                                                                                                          ctttctcc(n)ggaaaaaaaa
                                                                                                                                                                                                                                                                                                                                              actcaggcag(t)tcgagagcca
ctcaggcagt(t)cgagagccag
                                                                                 tttacaagta(n)aaaagagcat
                                                                                                                                                                                                                              ctaggaacct(n)cacctccttt
                                                         tgcactccag(n)attccagcct
                                                                                                                  aataaataat(n)caaagcagca
                                                                                                                                                                                                   teecetect(n)necetectee
                                                                                                                                                                                                                                                            ctcccacac(n)ctccccaccc
                                                                                                                                                                                                                                                                                        caccgtgcca(a)gcttatttt
                                                                                                                                                                                                                                                                                                                      ctcagcggag(n)aacagcctag
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus changing edits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary Statistics -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                          ctttctctc(t)ggaaaaaaaa
                                                                                                                                                                                                   ctaggaacct(g)cacctccttt
tccccctcct(c)cccctcctcc
                                                                                                                                                                                                                                                                                                                                              actcaggcag(g)gcgagagccagctcaggcag(g)gcgagagccag
                                                      tgcactccag(c)attccagcct
                                                                                 tttacaagta(a)aaaagagcat
                                                                                                                  aataaataat(c)caaagcagca
                                                                                                                                                                                                                                                            ctcccacac(c)ctccccaccc
                                                                                                                                                                                                                                                                                        caccgtgcca(g)gcttatttt
                                                                                                                                                                                                                                                                                                                      ctcagcggag(c)aacagcctag
                                                                                                                                                                                                                                                                                                                                                                                                          Edited+Context
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183812
0.000104921
0.0374023
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repeat\_region
repeat\_region

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> complement(6858. /rpt\_family="L2" 7524. .7663

/rpt\_family="LlME1"

complement(7666...7699)
/rpt\_family="AT rich"
complement(7700...7790)
/rpt\_family="Alu8g/x"
complement(7791...7832)

/rpt\_family="Alusc"
complement/7000"

/rpt\_family="AluSg/x"

repeat\_region
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/rpt\_family="MER77" 6295. .6461

/rpt\_family-"MER5B"

.7224)

/rpt\_family="MER57B"
complement(5509. .56)

5687)

rpt\_family-"AluJb"

.6160

/rpt\_family="AluSp"

/rpt\_family="MER4B" 1669. .4970 /rpt\_family="AluSx"

169146 169213 169214 176105 178686 183324	ttgttccant(n)atctgtgtct acattacatg(n)ncgggcgtgg cattacatgn(n)cgggcgtggt ctacaaatat(n)aaaattagca gaattggttt(n)gtggaagaca gtttgtttgt(n)ttgttttgtt  ttgttccaat(g)atctgttct acattacatg(g)cgggggtggt ctacaaatat(n)aaaattagca gaattggttt(c)gtggaagaca gtttgtttgt(n)ttgttttgtt
:	- Distribution of Quality < 40 Bases
bases	1000 900 900 800 800 700 700 800 800 800 800 800 8
	2000
	5 10 15 20 25 30 35 40 Phrap Value Range
Version: URES source	1.01 qxfo. Location/Qualifiers 1. 185161 /organism="Homo sapiens" /db_xref="taxon:9606"
repeat_region	Cione= krci+ bisbs; complement(1, .79) /rpt_family="Alus"
repeat_region	lement(80 _family='
repeat_region	_
repeat_region	
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repeat_region	28462885. /rpt_family="MER5B"
repear_redrou	/rnt familv="Aluso"

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RESULT 14
AC073530/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 101696 GTTTCATGTTCTTGTACACTTCCCCTCTGGGATCAGGTGAGGGGTCCAGACAGCTGACCA 101637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carzos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, C., Chen, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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AC073530.17 GI:13162369
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 161547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACU/333U 16154/ bp DNA HTG 28-FEB-2001 HOMO Sapiens chromosome 12 clone RP11-123010, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, 5 unordered pieces.
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/rpt_family="L1M4"
complement(10753. .11023)
/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(10378. .10411)
/rpt_family="(CA)n"
10424. .10497
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complement/10000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="L1ME1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alusq"
8464. .9146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (8162.
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/rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="L1ME3"
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1. .9712
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Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Tamerisa,K., Tang,H., Sutton,A., Yaylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usman,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Walliams,S., Walliams,G., Williamson,A., Washington,C., Washington,S., Walliams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
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Direct Submission

Direct Submission

Direct Submission

Submitted (22-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Feb 28, 2001 this sequence version replaced gi:13123810.
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Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 15% of reads
Chemistry: Dye-terminator Big Dye: 85% of reads
Assembly program: Phrap; version 0, 990329
Consensus quality: 160458 bases at least Q40
Consensus quality: 161972 bases at least Q30
Consensus quality: 161972 bases at least particle of the program o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: RP11-123010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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COMMENT

REFERENCE TITLE JOURNAL AUTHORS JOURNAL TITLE

source NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence be preserved as soon as it is available and the accession number will 156391 156491 157493 157593 158939 159039 /clone="RP11-123010" /db\_xref="taxon:9606" /chromosome="12" /organism="Homo sapiens" Location/Qualifiers 1. .161547 156390: contig of 156390 bp in length 156490: gap of unknown length 157492: contig of 1002 bp in length 157592: gap of unknown length 158938: contig of 1346 bp in length 159038: gap of unknown length 160260: contig of 1222 bp in length 160360: gap of unknown length 161547: contig of 1187 bp in length 31335 g 49855 t 415 others

BASE COUNT

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RESULT 15
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Burkett,C., Burrows,J., Control David B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J., Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Ouiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Marks, R., Stamps, A., Sucgang, R., Marks, R., Stamps, A., Stamps, A., Stamps, A., Stamps, M., Sapak, R., Marks, R., Stamps, A., Stamps, M., Stamps
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On Sep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 6% of reads
Chemistry: Dye-terminator Big Dye: 94% of reads
Assembly program: Phrap; version 0, 990329
Consensus quality: 156950 bases at least Q40
Consensus quality: 164968 bases at least Q30
Consensus quality: 170263 bases at least Q30
Consensus quality: 170263 bases at least Q50
Estimated insert size: 169417; sum-of-contigs estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: HAVK Center clone name: RP11-308L22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
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53.9%;
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Pred. No. 9.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bunac, C
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Query Match Best Local S Matches 52

l Similarity 52; Conserv

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Score 32.8; DI pred. No. 9.9; O; Mismatches

DB

74; Length 177765;

9.8%;

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BASE COUNT
ORIGIN
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                                                              source
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 24 contigs. The true order of the pieces
is not known and their order in this sequence record is
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Search completed: August 24, 2001, 03:54:00 Job time: 4216 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	No.	Score	Query Match	Query Match Length DB	!	ID	Description
	-	33	9.8	4217	21	AAC76650	Human ORFX ORF2205
o	N	31.2	9.3	3067	15	AAQ81157	Human EAA3c excita
C	w	30.6	9.1	1147	21	AAC36410	Arabidopsis thalia
O	4	30.6	9.1	1626	21	AAC40084	Arabidopsis thalia
	u	30.4	9.0	5534	14	AAQ35988	<ul> <li>Tomato hsp80 genom</li> </ul>
	σ	30.2	9.0	965	20	AAX20446	Human secreted pro
	7	30.2	9.0	1275	21	AAA62025	Hydrophobic domain
	8	30.2	9.0	1278	21	AAC93406	Human secreted pro
3	9	30.2	9.0	1712	21	AAA62035	Hydrophobic domain
	10	30.2	9.0	2171	21	AAA09354	G protein-coupled
	11	29.8	8.9	441	21	AAC02302	Human secreted pro

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27.4	27.4	27.4	27.4	27.6	27.8	28	28	28	28	28	28	28	28.2	28.2	28.2	28.2	28.2	28.4	28.4	28.4	28.4	28.4	28.6	29.2	29.4	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.8
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2834	2834	2302	1389	1322	49136	536165	534720	34263	34203	10732	3287	1399	4089	3621	3416	3416	849	7560	7346	7286	6744	2773	2921	49999	14784	2602	1246	1169	1169	1169	1166	$\vdash$	15914
10	œ	20	22	21	21	19	19	22	22	21	21	12	21	19	19	17	21	22	20	17	20	20	21	20	21	18	18	18	18	18	18	18	22
AAN90394	AAN70307	AAX86274	AAF67781	AAC33434	AAA27475	AAV30459	AAV30458	AAF74547	AAF74546	AAA10594	AAC98900	AAQ11843	AA236693	AAV17800	AAV40859	AAT30373	AAC49585	AAC83437	AAX77924	AAT14547	AAZ38125	AAZ22704	AAA30884	AAZ23901	AAA64141	AAT93309	AAT93286	AAT93284	AAT93283	AAT93282	AAT93285	AAT93294	AAF57269
Genomic DNA of hum	Sequence of human	DNA encoding a hum	Corynebacterium gl	Arabidopsis thalia	NIDDM1 region incl	Rhizobium species	Rhizobium species	Penicillium citrin	Penicillium citrin	Gene encoding a su	Human pancreatic c	Human lactoperoxid	Nucleotide sequenc		Human PYK-2 protei	Probin tyrosine ki	Arabidopsis thalia	Human tenascin-C.	Human tenascin cDN	Cytotactin gene.	Human FATP genomic	omonas	Mouse GFAT II codi	Human LOBO homolog	Nucleotide sequenc	Tomato mottle viru		mottle	mottle		Tomato mottle viru	Tomato mottle viru	Mouse RetL5 genomi

## ALIGNMENTS

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RESULT
AAC76650
                                      08-FEB-2001
Human ORFX ORF2205 polynucleotide sequence SEQ ID NO:4409
                                                                                                             AAC76650 standard; cDNA; 4217
                                    (first entry)
                                                                                                               ВP
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immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; hone damaemia; nocturnal haemoglobinuria; burn; wound; Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; thrombosis; bone damage; cartilage damage; antiinflammatory disease; coagulation; contraceptive; hypertension;

Homo sapiens.

WO200058473-A2

05-OCT-2000.

31-MAR-2000; 2000WO-US08621

31-MAR-1999; 99us-0127607

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XX AAQ811
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Best Local Similarity
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                                                                                                               Homo sapiens
                                                                                                                                                                                                  excitatory amino acid
                                                                                                                                                                                                                                                Human EAA3c excitatory amino acid receptor cDNA.
                                                                                                                                                                                                                                                                                                                          22-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                     AAQ81157;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ81157 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3399 gtttcatgttcttgtacacttcccctctgggatcaggtgaggggtccagacagctgacca 3458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4217 BP; 888 A; 1243 C; 1230 G; 856 T; 0 other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antidiabeti; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to which represent the human ORFX open reading frames 1 to 3161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GACAGCTCGTNTCATGATCGACTCGGACCC 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GCTGCATCTTTTTCTATGCTCTCCCTGCTGGCGGCTGATGGGAGATACAGGACAGCAAAACG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gacagcttgacagctggtcaagacggtcac 3488
                                                                                                                                                                      receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 3600-3603; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                    (first entry)
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99US-0127728.
2000US-0540763.
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                        Location/Qualifiers
418..3015
                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA; 3067 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%;
                                                                                                                                                                                         receptor; human EAA3 receptor;
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Pred. No. 0.49;
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                    Arabidopsis thaliana DNA fragment SEQ ID NO:
Hybridisation assay;
                                                   17-OCT-2000
                                                                            AAC36410;
                                                                                                     AAC36410 standard; DNA; 1147
                                                                                                                                                                 2965 TATTCTTCCGTGATTTGTATATGAATTCTCCAATAGC
                                                                                                                                                                                                                           3025
                                                                                                                                                                                                                                                                                                                                                 receptors.

N.B. The cDNA and corresp. amino acid sequences for EAA3b, 3c and 3d do not appear in full in the specification; the sequences have been compiled by combining sequences in Figures 1 and 4 according to the description given in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                         The human EAA3a receptor (AAR60112) and its variants EAA3b, EAA3c and EAA3d (AAR63068-R63070) occur naturally in human brain. They are all members of the EAA3 receptor family, having extracellular N- and C-termini and 4 internal hydrophobic domains which anchor the receptor within the cell surface membrane. The receptors bind glutamate and also exhibit binding properties characteristic of kainate-type EAA
                                                                                                                                                                                 176 GAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGC
                                                                                                                                                                                                                                        116 ATGITGNATICIATCAGCICACCCGTIGNTACAAGIGTAGNCICAAAGGAAGAATAGIGG 175
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1 and Fig 4B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide encoding a human excitatory amino acid 3 receptor or fragment - used to assay test ligands for their interaction with a human CBS receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elliot CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR63069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KAMB/) KAMBOJ R. (ELLI/) ELLIOT C E. (NUTT/) NUTT S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-1992;
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                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "encodes a truncated version of EAA3a in which 40 amino acids have been eliminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from the C-terminus and in which the las
11 amino acids differ from those in the
corresponding region of EAA3a"
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0; Mismatches
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genetic mapping; gene expression control;

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			ion; signal transduction promoter; termination section section.  a.  -0.0121825.
			rion pathway: n sequence; ss.
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07-SEP-1999; 10-SEP-1999;

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XX
DT 17-OCT-2000 (first entry)
XX
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XX
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                                                                                                                                                                    210 GCCCTGAGNTTCCAGAGGGNCCTGGTCG 238
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16-SEP-1999;
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                                                                                                                                                                                                                                                               CTTCTACTTCTTCAATCTCATCTTTTTCGATTTTGAACATCTCTGAATTAGATAACC
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Tomato hsp80 genomic clone Ghsp-4(locus A).
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'note= "Exon 2"
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/note= "Intron 1"
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1846..1856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                           WO9906423-A1
                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Pred. No. 4.1;
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19-AUG-1997; 30-JUL-1997; 30-JUL-1997;

97US-0056730. 97US-0054209. 97US-0054211.

29-JUL-1998;

98WO-US15949

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                                                                                                                                                                                                                                                                                                                  This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX20403) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 83 novel genes and their fragments (nucleic acid sequences: AAX20412-X20499; amino acid sequences AAX00258-Y00377) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in sea AAX70417 for described new in the new polynucleotides.
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18-AUG-1997;
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19-AUG-1997;
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30-JUL-1997;
30-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                       02-FEB-2001
                                                                  AAA62025 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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P-PSDB; AAY00292.
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Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                                                                                                                                                                                                                                                                cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
                               activin/inhibin activity, chemotactic/chemokinetic activity, haemcand thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                 protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity,
                                                                                                                                                                                                                                                                                                                                                                                                         Secretory proteins play important roles in the proliferation control, differentiation induction, the material transport and the biophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 303; 410pp; English.
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27-APR-1999;
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cancer via gene therapy.
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98JP-0364315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENT
                                                                                                                                         haemostatic
                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                    of.
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RESULT
AAC93406
ID AAC9
XX
                                                     В
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                                                                                       DЬ
                                                                                                       8
                                                                                                                                    Query Match
Best Local
                                                                                                                          Matches
         AAC93406 standard; cDNA; 1278
                                                     1034
                                                                                       974
                                                                      233
                          8
                                                                                                 TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC 232
                                                                       TGGTCGTCCCATCGCCTAGCAGGGTTC
                                                                                     tggtgggcacctcggcgggggtggtcc
                                                                                                                           50;
                                                                                                                                    Similarity
                                                                                                                           Conservative
                                                                                                                                  9.0%;
57.5%;
                                                                                                                          Score 30.2; E
Pred. No. 2.5;
0; Mismatches
                                                                                                                           0
         ВP
                                                     1060
                                                                       259
                                                                                                                                    5
                                                                                                                                             BB
                                                                                                                           37;
                                                                                                                                            Length
                                                                                                                           0,
                                                                                                                           Gaps
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Sequence 1275

BP;

162

Α,

417 C;

406 G;

290

Τ;

0 other;

0;

Hydrophobic domain protein cDNA HP10636 isolated from HT-1080 cells

Human secreted protein

gene

3

SEQ ID

NO:53

Q 밁

В

26-FEB-2001 AAC93406;

(first entry)

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CC AABS1722 represent human secreted polypeptide sequences and proteins CC invention. Human secreted proteins have activities based on the tissues CC and cells the genes are expressed in Examples of activities include: CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative; CC cytostatic; cardiant; vasotropic; cerebroprotective; notropic; creative; antibacterial; virucide; fungicide; and proteins mice of prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used CC pathological condition. Disorders which are diagnosed or treated include CC autoimmune diseases, hyperproliferative disorders, cardiovascular CC disorders, infections caused by bacteria, viruses and fungi and ocular CC disorders. The polypeptides can also be used to all wound healing and ce pithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of columentiaes can also he used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                        increase or decrease storage AAB51619 represent sequences
                                                       polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC93355 to AAC93363 and AAB51619 represent sequences which are used in the exemplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polynucleotide sequences given in AAC93364 to AAC93412 encode thuman secreted proteins given in AAB51620 to AAB51668. AAB51669 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB51662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1999; 99US-0128702.
20-JAN-2000; 2000US-0177049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cerebroprotective; nootropic; neuroprotective; antibacterial; viruc fungicide; ophthalmological; gene therapy; autoimmune disease; infenderproliferative disorder; cardiovascular disorder; angiogenesis; cerebrovascular disorder; nervous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000; 2000WO-US09069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200061620-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-619225/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN GENOME SCI INC
ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komatsoulis
                                                   exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection;
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RESULT
AAA62035
                         activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                     protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing
                                                                                                                                                                                                                                                                     Secretory proteins play important roles in the proliferation control, differentiation induction, the material transport and the biophylaxis cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various
                                                                                                                                 activity, haematopoiesis activity, tissue growth activity
                                                                                                                                                                                                                                         channels and transporters. The present sequence is the coding sequence to a human protein which has at least one hydrophobic domain. The
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biophylaxis; signal receptor; ion channel; transporter; immunostivulant; immunosuppressant; haematopolesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-1999;
27-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; membrane protein; hydrophobic doma
proliferation control; differentiation induction; material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA62035 standard; DNA; 1712 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB12142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAGAMI CHEM
PROTEGENE IN
                                                                                                                                                                                                                                                                                                                                                                                                       Page 321-324; 410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kimura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain protein cDNA HP10636 isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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99JP-0119299
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  gene
therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HT-1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain;
                                                                                                                                                          or suppressing
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of
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Sequence

1712

BP;

246 A;

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538

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376 T;

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173 TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC 232

Matches

Local

Similarity

9.0%;

Conservative

0,

37;

Indels Length

0,:

Gaps

0

Score 30.2; D Pred. No. 2.5; 0; Mismatches

DB

Sequence

1278

BР;

259

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355

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379

G; 278

T; 7 other;

present invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                  This sequence encodes human G-protein coupled receptor protein (GCRP) The GCRP polypeptides, polynucleotides, antibodies, antagonists and agonists may be administered to human patients for the diagnosis, treatment and prevention of nervous system disorders (e.g. epilepsy, stroke, neoplasms, Alzheimer's disease), autoimmune or inflammatory disorders, complications of cancer, hemadialysis and extracorporeal circulation, and cell proliferative disorders. They are also used to treat or prevent disorders associated with decreased or increased expression or activity of GCRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; antiasthmatic; antianemic; antiarteriosclerotic;
antithyroid; cytostatic; hepatotropic; dermatological; anti-inflammatory;
antigout; thyromimetic; haemostatic; virucide; hepatotropic; osteopathic;
                                                                                                                                                                                                        Novel human G-protein coupled receptor proteins used treatment and prevention of nervous system disorders, autoimmune/inflammatory disorders, and cell prolifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor protein 8 coding
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                                                                                                                                                                                                                                                                                                           Guegler KJ,
                                                                                                                                                                                                                                                                                                                         Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-1998;
06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200020590-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiparasitic; immunostimulant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCRP-8; G protein-coupled receptor protein; antipsoriatic; antirheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA09354
                                                                                                                                                                 Claim 9; Page 79-80; 84pp; English.
                                                                                                                                                                                                                                                                                 WPI; 2000-328934/28
                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1999;
                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 57.1 hes 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgggcgtgttctgtgggggctacctgatggcgctggcagtcctgagcccctgccccgcccc 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC
                                                                                                                                                                                                                                                                  AAY92368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                         Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                           Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                             98US-0167219.
98US-0172211.
99US-0133585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 568..1905
                                                                                                                                                                                                                                                                                                                         Lal .P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.5%;
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                                                                                                                                                                                                                                                                                                           Baughn
                                                                                                                                                                                                                                                                                                                        Bandman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
0; Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                         MR O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                         Au-oung
Azimzai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.9;
                                                                                                                                                                                                           cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
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                                                                                                                                                                                                                                   the diagnosis,
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                                                     They are
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Query Match

.0%;

Score

30.2;

DB

21;

Length 2171;

밁 Qy

38

167 GAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGA 226

gagtattcccactttcctgtgcggtgcagcagtatgcctgggggaagatgggttccaaca

Matches

Query Match Best Local

Local

1 Similarity 76; Conserv

Conservative

0;

90;

Indels

Gaps

0

8.9%; 45.8%;

Score 29.8; DE Pred. No. 2.2; 0; Mismatches

DВ

Length

441; 0

Sequence

2171

BP;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                     derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1661
                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo diagnostic, forensic, gene therapy and chromosome mapping procedu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                            Claim 1; SEQ ID 2300; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC02302 standard; cDNA; 441
Sequence
                                                                                                                                                                                                                                                                                                                                                                          Dumas
                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET
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441
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ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; secreted protein; cDNA isolation;
phromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0122487
102 A; 130 C;
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                                                                                                                                                                                                                                                                                                                                                                          Duclert
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 122
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Mismatches
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                                                                                                                                                                                                                                                                        mapping procedures
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cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic
                                                                                                                                                                                                                                                                       Ret ligand 5; RetL5; autophosphorylation; tumour; renal; nephrotropic; Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
                                                                                                                                                                                                                                                                                                            Mouse RetL5
                                                                                                                                                                                                                                                                                                                                                        AAF57269
                                                                                                                                                                                                                                                                                                                                                                           AAF57269 standard; DNA; 15914 BP
                                                                                                                                                                                                                                                                                                                                  29-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGNCCTGGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGCNCATGGCAGTC
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01-SEP-2000; 2000WO-US24111

01-SEP-1999; 99US-0152024

(BIOJ ) BIOGEN

Worley

2001-235091/24

Novel Ret ligand polypeptide useful for suppressing growth of a tumor cell that expresses Ret and for modulating Ret signal transduction involving a cell expressing Ret polypeptide or Ret ligand polypeptide

Claim 1; Page 42-53; 76pp; English

The invention relates to mouse and human Ret ligand 5 (RetL5) polypeptides. The RetL5 polypeptides can be expressed by standard recombinant methodology. The RetL5 when bound to Ret, acts as a dimerization or autophosphorylation activator. The polypeptides and their antibodies are useful for stimulating growth of or limiting damage to, Ret expressing tissue in a subject, for suppressing growth of a tumour cell that expresses Ret, for modulating Ret signal transduction involving a cell expressing the Ret polypeptide. The RetL5 polypeptides, fusion proteins containing RetL5 and antibodies are useful for stimulating renal tissue growth and/or survival, supporting renal function and minimizing damage to renal tissue after various insults, particularly for treating acute renal failure, acute nephritis, chronic renal failure, nephrotic syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic injury and trauma. The compounds are also useful for treating conditions are also useful for treating conditions. such as neural degeneration where neural growth and regeneration are desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's diseate, the desirable of the state of the sta tissue caused by neoplastic impingement, trauma or cerebrovascular events such as hemorrhage or emboli, and neural disorders such as mental retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral motor neuron disease, demyelinating disease, bacterial diseases, viral diseases, and prion diseases including Creutzfeldt-Jakob disease. The compounds are also useful for treating disorders due to damage to neural palsy. The present sequence genomic DNA sequence 0

infection

transgenic plants

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                    DNA-B. It encodes a protein (see AAW34336) having a DNA binding site specific to the DNA-A common region, a DNA nicking activity, and an NTP binding activity. The invention involves production of transgenic plants containing DNA comprising AC1 or C1 wild-type or mutant sequences that negatively interfere in trans with
                                                                                                                                                                                                                                                                                                                                                                                Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
                                                                                                                                                            that has a bipartite genome. The AC1 gene must be exefficient replication of the two genomic components,
                                                                                                                                                                                                                   wild-type AC1 gene
                                                                                                                                                                                                                                                This genomic DNA sequence includes the open reading frame
                                                                                                                                                                                                                                                                                                        Example 3.3;
                                                                                                                                                                                                                                                                                                                                                               golden mosaic geminivirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT93294;
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(WISC ) WISCONSIN ALUMNI RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT93294 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s; ToMoV; AC1 ge
plant; disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                        Page 57-58; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                      of tomato mottle virus (ToMoV), a geminivirus te genome. The AC1 gene must be expressed for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%;
46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; transdominant mutation;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss; cyclic; circular
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                                                                                                                                                               DNA-A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3479
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Best Local
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This DNA sequence comprises a mutated ACl gene of tomato mottle virus (TOMOV). It carries an inserted 4-base Sau3A site that shifts the ACl gene translation reading frame resulting in the expression of a truncated ACl protein (see AAW34327). The ACl gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome. The invention involves production of transgenic plants containing DNA comprising geminivirus ACl or Cl wild-type or mutant
                                                                                                                                                                      Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
                                                                                                                                                                                                                                                                                                     (SEMI-)
                                                                                                                                                                                                                                                                                                                                                                            15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geminivirus; ToMoV-Acidlm23; AC1 gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are resistant to viral infection. The AC1/C1 genes are especially from ToMoV, tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AAM33282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking domain and/or the NTP-binding domain.
                                                                                                                                Claim 11; Page 72-73;
                                                                                                                                                                                                                                 WPI; 1997-526447/48.
P-PSDB; AAW34327.
                                                                                                                                                                                                                                                                                                                                              16-APR-1996;
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                                                                                                                                                          golden mosaic geminivirus
                                                                                                                                                                                                                                                                          Ahlquist PG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomato mottle virus isolate Florida
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virus (ToNov). It encodes an ACI protein (see AAW34324) that carri mutations in its NTP-binding domains. The ACI gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A-and DNA-B, of the bipartite ToMoV genome.

carries

This DNA sequence comprises a transdominant lethal mutant, designated ToMoV-AC1dlm, of the AC1 gene of tomato mottle virus

Claim 11;

Page

60-62; 132pp; English.

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RESULT :
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                Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
                                                                                                                                                                                                                                                                                                                                                                                       CDS
golden mosaic geminivirus
                                                                                        P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geminivirus; ToMoV-Acldlm; ACl gene;
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                                                                                        AAW34324.
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Search completed: August 24, 2001, 03:53:37 Job time: 1418 sec

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US-08-314-309A-2
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US-08-314-309A-1
US-08-634-634-1
US-08-634-501-1
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US-09-422-869-1
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7.6 11088 4 7.6 1128 4 7.6 1875 4 7.6 2303 2 7.6 2303 2 7.6 2308 2 7.6 2308 2 7.6 2421 3 7.6 2421 3 7.6 25221 4 7.6 2008 2 7.6 2008 2 7.6 2008 2 7.6 2008 2
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ALIGNMENTS

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RESULT 1
PCT-US95-11684-1/c
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                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11684
FILING DATE: 14-SEP-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308/359
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN INFORMATION:
REFERENCE/DOCKET NUMBER: 33,950
REFERENCE/DOCKET NUMBER: BEC0019P
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING SAME
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                        FEATURE:
                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 10666 NOTIFY: La JOlla STATE: CA COUNTRY: USA
NAME/KEY: CDS
LOCATION: 55..665.
OTHER INFORMATION:
                                                                                                                   LENGTH: 7286 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: The Scripps Research Institute, Office ADDRESSEE: Patent Counsel STREET: 10666 North Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: USA
92037
                                                                                               DNA (genomic)
                         .6654
  /product= "cytotactin"
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                                                              Matches
                                                                                         Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-357-642A-2/c
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ENERAL INFORMATION:
   1152
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sima Lev
APPLICANT: Joseph Schlessinger
APPLICANT: PYK2 RELATED PRODUCTS
                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4850 GAGACCATAACCTCATAGCC 4831
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                           114 CTATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTAGNCTCAAAGGAAGAATAGT 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 ATCTGAATCCCCGNNTGGCC 213
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                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 CATGATCGACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTTGNATTCTATCAGC 133
                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: Decemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                               TELEFAX:
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ZIP: 90071-2066
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STREET: Suite 4700
                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
CTATGAGGTCAGCCATGTTCTCAGCCTCTGCTAGGGATGAGGTTTTGATGGACAAGGCCT 1093
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                                                              54;
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67-3510
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                                                             Conservative
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48.6%;
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52.9%;
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                                                                           Score 28.2; D
Pred. No. 2.4;
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Pred. No. 3.
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                                                         Mismatches
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                                                                                        DB 2;
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                                                             48;
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                                                                                        Length 3416;
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                                                                                                                                                               Query Match
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                                                                  1152 CTATGAGGTCAGCCATGTTCTCAGCCTCTGCTAGGGATGAGGTTTTGATGGACAAGGCCT 1093
1092 GGGGGGCACCTTCAATGCCCAGCTGAAGTACTGCCTGGCCCT 1051
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1092 GGGGGGCACCTTCAATGCCCAGCTGAAGTACTGCCTGGCCCT 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SIMA LEV
APPLICANT: JOSEPH SO
                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                   174 GGGÄGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCT 215
                                                                                                114 CTATGTTGNATTCTATCAGCTCACCCGTTGNTACAAGTGTAGNCTCAAAGGAAGAATAGT 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08 FILING DATE: June 2, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                       TELEX:
                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 633 West Fifth
STREET: Suite 4700
                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                   nucleic acid
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67-3510
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AVENTION: PYK-2 RELATED PRODUCTS AND
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                                                                                                                                 Conservative
                                                                                                                                                                                                                                     linear
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                                                                                                                                                 52.9%;
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                                                                                                                                Score 28.2; DE Pred. No. 2.4; 0; Mismatches
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                                                                                                                                                               DB 2;
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                                                                                                                                                                   Length 3416;
                                                                                                                                 Indels
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                                                                                                                                Gaps
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US-09-422-869-1

GENERAL INFORMATION:

APPLICANT: POLONSKY, KENNETH S.

Sequence 1, Application US/09422869 Patent No. 6235481

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match (8.3%; Best Local Similarity 53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIGH L
APPLICANT: BELL, GRAEME I
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SREENAN, SEAMUS
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                                                       REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 49136
                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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ZIP: 98121
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2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                            USA
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Havukkala, Ilkka
                                          206-269-0563
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Pred. No. 15
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                                                                                                                                             US-08-975-316-3
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                                                               Matches
                                                                            Query Match
Best Local Similarity
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Best Local Similarity
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APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: September 11, 1996 ATTORNEY/AGENT INFORMATION: NAME: SLEATH, Janet
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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               232 CTGGTCGTCCCATCGCCTAGCAGGGGTTCAAGNAAAGGGGCCCGCNCATGGCAGTCCTTGG 291
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OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
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Pred. No. 2.7;
                                                                              Score 27.2;
Pred. No. 2.
                                                               Mismatches
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Best Local Similarity 50.5%;
Matches 53; Conservative
     APPLICATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/699
APPLICATION TO NUMBER: 08/699
APPLICATION NUMBER: 08/699
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J
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LOCATION: (463)...(463)
-09-211-710-3
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APPLICANT: Grierson, Alastair
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin (
FILE REFERENCE: 11000.1003c3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
EQ ID NO 3
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                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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ORGANISM: Pinus radiata
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                            CITY: Palo Alto
                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304-1013
                                                                                                                                                                                                                                                                                               STREET:
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925 Page Mill Road
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                                                                                        US/08/911,853
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Pred. No. 2.7;
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US-09-479-409-6
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Best Local (
                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATA:
PRIOR APPLICATION DATA:
08/911,853
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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LENGTH: 1512 base pair
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REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
                                                         STRANDEDNESS:
                                                                                                                                                                            TELEPHONE: 650-845-6504
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                                                                                                                                                                                                                                                                                                                                      NAME: Glaister, Debra REGISTRATION NUMBER: :
                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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925 Page Mill Road
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Pred. No. 3.
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Query Match

Best Local Similarity

8.1%; 60.3%;

Score 27.2; D Pred. No. 3.5;

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Best Local S
Matches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
                                                                                                                                                                              1041 CTGGTTCCGTTATCTGCACGCCTGGTCCAAGAACAGCGTCCAGCTCTGCGCGCACCTTGC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, ILANG APPLICANT: and GRIESSON, ALASTAIR W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 206-269-0565
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                                                                                                             981 TCTGAATGTCCTGGTGGTTCACCAGCTCCGCTATTCCCCATTCCA 937
                                                                                                                                             292 NCAGNAGNAANGGANTTGGNCCCAACCCCNTTGGTTCCCAACCCA 336
                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                Local Similarity
les 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 37,007
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                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                             CTGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCCGCNCATGGCAGTCCTTGG 291
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2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206-269-0563
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RESULT 12
US-09-479-409-29
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Best Local Similarity
                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     11077
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ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/6
FILING DATE: 16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                               APPLICANT: Gerritse, Gijsbert APPLICANT: Quax, Wilhelmus J.
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                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                          173 TGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGNNTGGCCCTGAGNTTCCAGAGGGNCC 232
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                                             COUNTRY:
                                                              STATE:
                                                                           STREET: 925 Pag
CITY: Palo Alto
                                                                                         ADDRESSEE: Genencor International STREET: 925 Page Mill Road
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94304-1013
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                                                      CA
                                                                                                                                                                                                                                          Application US/09479409
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Diskette
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37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27.2;
Pred. No. 14;
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                                                                                                                                                 SYSTEM FOR ALTERED LEVELS
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Gaps

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CURRENT APPLICATION DATA:

OPERATING SYSTEM:

IBM Compatible

APPLICATION NUMBER: US/09/479,409

FILING DATE:

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                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Homo sapiens US-09-087-465-3
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                                                                                                                                      Matches
                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              SEQ ID NO 3
LENGTH: 17949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09087465A Patent No. 6160092
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/087,465A CURRENT FILING DATE: 1998-05-29
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Darnell Jr., James E
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF
TITLE OF INVENTION: USE
                                                              12998 aaaaaaaaaaagtgctgttcatctgtgtgatctcactgaatcttcgtacttcaaaccct 13057
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 600-1-229
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, Xiaomin
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vinkemeier, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11077
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                                                                                160 AAAGGAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGUNTGGCCCTGAGN 219
                               220 TTCCAGAGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGCNCAT 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 TGGTCGTC 240
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REGISTRATION NUMBER: 33,888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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47.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29:
                                                                                                                                                Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27.2;
Pred. No. 1
                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                DB 4; Length 17949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 17612;
                                                                                                                                 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                 Indels .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                             Gaps
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Qγ
Query Match
Best Local Similarity
Matches 63; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (203) 254-11 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13118 ggcagggcttggtccaaag 13136
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1329 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Klee, Maurice M.
                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Dell 486/50
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WORDERFECT 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                               TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                         VOLUME: 64
PAGES: 5491-5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Klee, Maurice M
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GGCAGTCCTTGGNCAGNAG 298
                                                                                                                                      JOURNAL:
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: July
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Fairfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                           RS: Massey, A. C.
RS: Coppola, M. A.
RS: Thomas, C. Y.
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determinants of recombinant
determinants of recombinant
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                                                                                                                                                                xenotropic viruses from CWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1951 Burr Street
                                                                                                                                    Journal of Virology
                                                                                                                                                                                                                                                                                                  No
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                                                                                                                                                                                                                                                                                                                                                             Linear
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                                                                                                                                                                                                                                                                                                                  No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maurice M. Klee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (203)
                                                                                                                                                                                                                                                                                                                           cDNA to genomic
Xenotropic gp70
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                                                                                                                                                                                                                                                                                                                                                                      Single
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                  7.98;
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   Score 26.4; DI
Pred. No. 6.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                            protein
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                             DB 1;
                             Length 1329;
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Conservative

0;

65;

Indels

0; Gaps

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; TOPOLOGY: 11r; MOLECULE TYPE: ; MYDOTHETICAL: NO ; ANTI-SENSE: NO US-08-848-810-1
Search completed: August 24, 2001, 03:51:27 Job time: 2333 sec
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US-08-848-810-1
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 54; Conserv
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Patent No. 6074851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 616-833-6897
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Deibel JI
APPLICANT: Yem, A. V
APPLICANT: Wilson, of
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WOOLLON, Thomas A.
REGISTRATION NUMBER: 35,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-7914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN ReLease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,810
FILLING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   638 CGCAGGGAAGCCTTTGCCCAGAGACCCAGCTCGGCCCCCGACCTGATGTGT 688
                                                                                                                                                      578 GAGCTGCCAGCAGCTCTGGGGAATCCCAGCTCCACCCATGCTCTGGCAGAGTGGGCCAGC 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 GGGAAGAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 TGNTACAA 149
                                                                                                                    276 NCATGGCAGTCCTTGGNCAGNAGNAANGGANTTGGNCCCAACCCCNTTGGT 326
                                                                                                                                                                                      216 GAGNTTCCAGAGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAAGNAAAGGGGCCCGC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 ACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTTGNATTCTATCAGCTCACCCGT 141
                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49001
                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08848810
                                                                                                                                                                                                                                                                                                                                                                                                                               2890 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pharmacia & Upjohn Company
301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deibel Jr., M. R.
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                CDNA
                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                        7.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catalytic Macro Molecules 
Like Activity
                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                        Score 26.4;
Pred. No. 10;
                                                                                                                                                                                                                                                          DB 3; Length 2890;
                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Having DCD25B
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                        0;
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em\_esthum21:\*
em\_esthum22:\*
em\_esthum23:\*

em\_esthum13:\*
em\_esthum14:\*
em\_esthum15:\*
em\_esthum16:\*
em\_esthum17:\*

em\_esthum18: em\_esthum19:

em\_esthum20:\*

em\_esthum10:\*
em\_esthum11:\*
em\_esthum12:\*

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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336
1 CGCTGCATCTTTTTCTATGC.....CCCCNTTGGTTCCCAACCCA 336
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Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est6:*
gb_est7:*
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gb_est5:*
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                                                               em_esthum5:*
em_esthum6:*
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    gb_est11:
    gb_est12:
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    gb_est28:
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em_esthum2:*
em_esthum8:*
em_esthum9:*
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em_esthum4:*
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em\_estpl1: \*
em\_estpl2: \*
em\_estpl4: \*
em\_estpl5: \*
em\_estpl6: \*
em\_estpl6: \*
em\_estpl8: \*
em\_estpl9: \*
em\_estpl10: \*

em\_estom2:\*
em\_estov1:\*
em\_estov2:\*

em\_estin3:\*
em\_estin4:\*
em\_estin5:\*
em\_estom1:\*

em\_estin1:\* em\_estin2:\*

em\_esthum28

em\_esthum24:\*
em\_esthum25:\*
em\_esthum26:\*
em\_esthum27:\*

94: 95: 96: 97: 98: 99: 100: 101: 102: 103:

em\_estro19:\*
em\_estro20:\*
gb\_est25:\*
gb\_est26:\*
gb\_est27:\*
gb\_est28:\*
gb\_est28:\*
gb\_est28:\*
gb\_est31:\*

gb\_est41: \*
gb\_est44: \*
gb\_est44: \*
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em\_estro10:\*
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gb_est111:*
gb_htc:*
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is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

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REFERENCE
- AUTHORS
                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
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AV607888/c
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3', mRNA
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            Bovidae; Bovinae; Bos.
1 (bases 1 to 509)
Sugimoto, Y., Hirotsune, S.,
                                                     COW.
                                                           AV607888.1
EST.
bovine cDNA sequencing
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                              Bos taurus
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Bos taurus kidney fetus
sequence.
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                                                                                                                              ALIGNMENTS
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             Takasuga, A.,
                                                                                      Bos taurus
              Itoh, R.,
                                                                                     30-AUG-2000
CDNA clone E1KI043F08
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AA234493 zr74h07.r
BF076427 22500
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AA017985 mh48f08.r
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BF325039 su1Bg10.y
BF077799 227942 MA
BF077938 229798 MA
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AI856977 MBNAAd-0.5
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AW755387 sl03d01.y
AW596813 sj83a05.y
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BG472715 602514536
BE378752 601237207
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AV663492 AV663492
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BB040208
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BE032856 132939 MA
BE121364 UI-R-CA0-
             Jitohzono, A. and
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BF394149 UI-R-CA0-
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AV663493
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                                                                                           bovine cDNA sequencing
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1 (bases 1 to 539)
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                                                                                                                                          Bos taurus
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/organism="Bos taurus"
/db_xref="taxon:9913"
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Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                Single pass sequencing.
This clone was obtained from a
                                                                                                                                                                             Unpublished (2000)
Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing.
This clone was obtained from a Location/Qualifiers
                                                                                                                                                                                                                                                       Sugimoto, Y., Hirotsune, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: kazusugi@cocoa.ocn.ne.jp
                                                         Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DH10B"
/note="Vector: pzil; Site_1: Sall; Site_2: Not1; Poly A
was deleted from a Not1 site"
ull c 157 g 110 t 1 others
Location/Qualifiers
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/db_xref="taxon:9913"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                    polyA-deleted cDNA library
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                                                                                                                                                                                                                                                           Jitohzono, A.
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Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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AV663814
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This clone was obtained from a polyA-deleted cDNA library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COW.
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    Conservative
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                                                                                                                                                                                                                                                            : kazusugi@cocoa.ocn.ne.jp
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/note="Tweetor: pZL1; Site_1: Sal1; Si
was deleted from a Not1 site"
7 a 133 c 123 g 126 t
                                                                                 Q
                                                                                                                 /Organism="Bos taurus"
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/clone_lib="Bos taurus b
/tissue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
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                                                                                                     /note="Vector: p2L1; Site_1: Sal1;
                                                                            deleted from a Not1 site" 144 c 129 g 128 t
              24.4%;
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  Score 82; DB 32; Length 539; Pred. No. 4.3e-15; 0; Mismatches 11; Indels
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Pred. No. 4.3e-15;
0; Mismatches 11
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3951
Fex: 81-438-52-3952
Fex: 81-438-52-3952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Takao Isogai
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HRI human cDNA project
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/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME185FL3"
207 c 197 g 180 t
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 900)
Li,W.B., Gruber,C., J
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                                                                                                                          mRNA sequence.
AL541183
                                                                                                                                                       AL541183 900 bp mRNP
AL541183 LTI_FL002_PL1 Homo
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Unpublished (2001)
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Mammalia; Eutheria; Primates;
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AL537924 LTI_FL013_FBrn1
prime, mRNA sequence.
AL537924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email: Fliangelifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="rrI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception
week, 24 week and 26 week)"
/lab_host="DH10B"
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51 c 224 g 245 t
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Libraries and normalization
                             Chordata;
Primates;
 Jessee, J.
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Pred. No. 6.8e-14;
1; Mismatches 13
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 and Polayes, D.
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Genoscope - Centre National de Su
BP 191 91006 EVRY cedex - France
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           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 66 row: K column: 23
Seg primer: ATTTAGGTGACACTATAG
                                                                                                 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                 USDA, ARS, US Meat Animal PO Box 166, Clay Center, Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                     pig.
Sus scrofa
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                                                                                                                                                   Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                             EST discovery
Unpublished (2
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                                                           FORWARD: AGGAAACAGCTATGACCAT
                                                                        PCR PRimers
                                                                                     and -minmatch 12 options.
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                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized
                                                                                                                                                                                                                                                                               and Keele,J.W.
                                                                                                                                                                                                                                                                                            Stone, R.T.,
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/db_xref="taxon:9606"
/clone="CSODE005YD14"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onote-*Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email:
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Pred. No. 8.
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8.9e-14;
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                                                                                                                                                                                                                                                                                                                                                  Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of seque
is likely internal to the message. cDNA Library Preparation: M.E
Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                        Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat.
Rattus norvegicus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE121364 435 bp mRNA EST 13-JUN-2000 UI-R-CA0-bax-a-08-0-UI.S1 UI-R-CA0 Rattus norvegicus cDNA clone UI-R-CA0-bax-a-08-0-UI 3', mRNA sequence.
BE121364 BE121364.1 GI:8513469
                                                                                                                                                                                                                                                                                                                     Research Genetics (www.resgen.com)
Seq primer: M13 Forward
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Bonaldo, M.F., Lenno
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              /lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CA0 library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library
                                                                                                                                                         /strain="sprague-Dawley"
/db_xxef="taxon:10116"
/clone="UI-R-CAO-bax-a-08-0-UI"
/clone_lib="UI-R-CAO"
                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2:
Library made from pooled tissue from day 11, 13,
and 30 embryos."
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/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
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/lab_host="DH10B"
which this clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lennon, G. and Soares, M.B.
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88.1%;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches
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Rattus norvegicus
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/Clone_"ULT CANO"
/Clone_Tib="ULT CANO"
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TAG_SEQ-None found"

a 106 c 114 g 115 t
                                                                                                                                                                                                                                                                                                                                                         /clone="UI-R-CA0-bhe-c-02-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                    /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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80.5%;
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Pred. No. 5.2e-09;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.ulowa.edu

Email: msoares@blue.weeg.ulowa.edu

Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                    Soares Lab Clone distribution: clo
Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 Eckstein Medical Research
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, M.F.,
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                  POLYA-NO
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              /lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAO
library is a subtracted library derived from the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_SEQ-None found"
106 c 114 g
site at ratest.eng.uiowa.edu. To previously described in (Bonaldo,
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                                                                                                                                                                                                                                   /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                           /clone_lib="UI-R-CAO"
                                                                                                                                                                                                               /clone="UI-R-CA0-bha-c-12-0-UI"
                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        791-806 (1996)
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Matches Query Match

Local

Similarity

16.7%; 84.9%;

Score 56; DB 175; Pred. No. 7.1e-07;

DB 175;

Length 711;

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BG293757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
Plate: LLAM10371 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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Location/Qualifiers
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   /db_xref="taxn:10090"
/db_xref="taxn:10090"
/clone="IMAGE:4502603"
/clone_tib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="PH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;
/note="
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TAG_SEQ=None found"
106 c 117 g 118 t
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Rodentia;
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RESULT 13
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AV663813/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERENCE
                                                                                                                                                                                                               414 ACAGCAAAACAGAGAGCTCAT-TCATGATGGACTCGGATCCTCAACG-CTGCATGAGGCA 357
                                                                                                                                                                         356
                                                                                                                                                                                              111
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                                                                                         BF300893 938 bp m
602028894F1 NCI_CGAP_SG2
                                                                                                                                                                                                                                                                    63;
                      Mus musculus
                                                          BF300893.1
                                                                        BF300893
           Eukaryota;
                                    ouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bovine cDNA sequencing Unpublished (2000)
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AV663813 Bos taurus brain fetus
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugimoto, Y., Hirotsune, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos. 1 (bases 1 to 414)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
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                                                                                  sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone was obtained from a polyA-deleted cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81-248-25-5725
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                                                                                                                                                                                                                                                                                                                                     /note="Vector: pZL1; Site_1:
was deleted from a Not1 site"
112 c 133 g 82 t
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/clone="E1BR038G07"
/clone_lib="Bos taurus brain fetus"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
          Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                          'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                       'dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Bos taurus"
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Pred. No. 1
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                                                                                              musculus
      Craniata; Vertebrata; Euteleostomi;
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                                                                                            CDNA
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                                                                                           clone
                                                                                                                                                                                                                                                                                      Length 414;
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                                                                                         IMAGE:4164238 5'
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AUTHORS
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JOURNAL
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On Jun 5, 1998 this
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68; Conser
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Mammalia; Eutheria;
                                                                                                                                                                                   Norway rat.
                                                                                                                                                                                                            AA998476.1
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                                                                                                                                                               Eukaryota;
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Eckstein Medical Research Building Iowa City,
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                                                                                                                                                 Chordata;
Rodentia;
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806 GAAAGAAGTCCGCCCCCTGGGAAACCATTGGAATGAGATAAGCAGTTGCCCCAGAAGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 CCCCGNNTGGCCCTGAGNTTCCAGAGGGNCCTGGTCGTCCCATCGCCTAGCAGGGTTCAA 261
                                                                                                                                                                     1 (bases 1 to 330)
1 (bases 1 to 330)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                               Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA998476 330 bp mRNA EST UI-R-C0-ie-a-08-0-UI.S1 UI-R-C0 Rattus norvegicus UI-R-C0-ie-a-08-0-UI 3', mRNA sequence.
                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN9449 row: k column: 23
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian Gene Collection
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/clone_lib="NCI_CGAP_GC;"
/clone_lib="NCI_CGAP_GC;"
/lab_host="DH10B_(T1 phage=resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: sali; Cloned unidirectionally. Primer: Oligo
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 209 c 267 g 237 t 1 others
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1 to 938)
                                                                                                  sequence version replaced
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Sciurognathi; Muridae;
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IA 52242, USA
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AA997859/c
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                                                                                                                                                                                                                                                                                                                                                                   199 GGAGACTTGAACTTTCAGGACCAGAATGAGGCAGCGGCAGGAGGATTGCTGCCAGCTTGC 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                   78 ATCGACTCGGACCCTCTGCGNCTGCATGAGGCACCACTATGTTGNATTCTATCAGCTCAC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 TGCTCTCCCTGCTGGCGCTGATGGGAGATACAGACAGCAAAACGGACAGCTCGTNTCATG 77
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AA997859 519 bp mRNA EST UI-R-CO-hu-c-11-0-UI.s1 UI-R-CO Rattus norvegicus UI-R-CO-hu-c-11-0-UI 3', mRNA sequence.
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//lab_host="DHIOB (Life Technologies)"
//note="vector: pf773D-Pac (Pharmacia) with a modified
//note="vector: pf773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Bco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-Al
and UI-R-E1 libraries. The UI-R-A1 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placentd, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-E1
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified cDNA inserts from a
pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the pooled UI-R-A1 and UI-R-E1 library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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/clone_11b="UI-R-CO"
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Pred. No. 1.6;
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Query Match 10.6 Best Local Similarity 54.4 Matches 68; Conservative

10.6%;

Score 35.6; DE Pred. No. 1.8; 0; Mismatches

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Length 519; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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Mammalia; Eutheria;
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AA997859.1
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Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                            embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-Al and UI-R-El clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-Al and UI-R-El library in the form of single-stranded circles. The remaining single-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and UIR-El libraries. The UIR-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UIR-El library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day
                                                                                  bacteria (Life Technologies) to generate the UI-R-C0
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
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/lab_host="DH10B (Life Technologies)"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_I: Not I; Site_Z: Eco RI; The UI-R-CO library is a subtracted library derived from the UI-R-Al
                                                              1996)"
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/db_xref="taxon:10116"
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Maximum DB seq length: 2000000000
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336
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gb_ov:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 654321	Result
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1769 1774 1846 1872 119945 162409 1493 1792	Length
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MMNDP MMNORRIE HSNDPG HSCHRX HSA218J18 AC022184 BC006263 AF236018	SUMMARIES
X83794 M.musculus X932397 M.musculus X932397 M.musculus X65882 H.sapiens m X65724 H.sapiens D AL034370 Human DNA AC022184 Homo sapi BC006263 Homo sapi BC006263 Homo sapi	Description

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                                      Submitted (05-JAN-1995) z. Chen, Molecular Neurogenetics Lab, Massachusetts General Hospital-East, Building 149, 13th Stree Charlestown, MA 02129, USA Location/Qualifiers
                                                                                                                                                                                    M.musculus NDP gene. x83794
                                                                                                             Characterization and mapping of
                                                                       Direct Submission
                                                                             Chen, Z
                                                                                            96432457
                                                                                                                         Chen, Z.Y.
                                                                                                                          Battinelli, E.M., Boyd, Y., Craig, I.W., Breakefield, X.O. and
                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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NDP gene; Norrie disease locus.
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                                                                                                  Genome 7
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X97675 H.sapiens m
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1 M.musculus mRNA for N

X92397

X92397.1 GI:11776.1
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Direct Submission
Direct Submission
Submitted (17-OCT-1995) W. Berger, MPI fuer Molekulare Genetik,
Ihnestrasse 73, D-14195 Berlin, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Northand Chases 1 to 1774)

Berger, W., van de Pol, D., Bachner, D., Oerlemans, F., Winkens, H., Hameister, H., Wieringa, B., Hendriks, W. and Ropers, H.H. An animal model for Norrie disease (ND): gene targeting of the
                                                                                                                                                                                                                                                                                                                                                                                            Hum. Mol. Genet. 5 (1), 96381426
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226. .599
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                                                                 youn(432. .599,600. .827)
/gene="ND"
                                                                                                                                                                                                                        /organism="Mus musculus"
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/db_xref="taxon:10090"
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                                                                                                                                                                               /tissue_type="brain'
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429...824
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X65882 S61557
X65882.1 GI:35016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (28-APR-1992) Z. Chen, University
Lab/Dept of Biochemistry, South Parks Road,
2 (bases 1 to 1846)
                                                                                                                                                                                                                                                                                                                                                                                            Nat. Genet. 1 (3), 204-208 (1992) 93265104
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen, Z.Y., Hendriks, R.W., Jobling, M.A., Powell, J.F., Breakefield, X.O., Sims, K.B. and Craig, I.W.
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1 (bases 1 to 1846)
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Query Match

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Score

22;

DB 93;

Length 1846;

RESULT 5 HSA218J18/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-APR-1992) W. Berger, University Hospital Nijmegen, Dept of Human Genetics, Geert Grooteplein 20, P.O.Box 9101, 6500 HB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berger,W., Meindl,A., van de Pol,T.J., Cremers,F.P., Ropers,H.H., Doerner,C., Monaco,A., Bergen,A.A., Lebo,R., Warburg,M. et,al. Isolation of a candidate gene for Norrie disease by positional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1872)
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                                                                                                                                                         /protein_id="CAA46640.1"
/db_xref="GI:1335017"
/translation="RHGGCDAGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
/translation="RHGGCDAGACDSLPSTGTSSPVTARNAIPEARCCVWLLDGTTV
EAVRPARERLAKKELROKRMODFSRDSAYSSNKDSTCLLTERDTLGTSLOFESPFSGT
ISFGSFSDSGIFPLGSCOCLGFQDFSISGKKWALIHKRVRLSVFGARWGRIYFGK"
1 425 c 409 g 517 t
                                                                                                                                                                                                                                                                                                                            /codon_start=1
/protein_id="CAA46639.1"
/protein_id="CAA46639.1"
/db_xref="GI:29947"
/db_xref="SWISS-PROT:000604"
/translation="MRKHVLAASFSMLSLLVIMGDTDSKTDSSFIMDSDPRRCMRHHY
VDSISHPLYKCSSKMYLLAARCEGCHSGASRSEPLVSFSTVLKQPFRSSCHCCRPQTSK
VDSISHPLYKCSGMRLTATYRYILSCHCEECNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="adult and fetal retina libr." /map="p11.4" 417. .818
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/db_xref="taxon:9606"
/chromosome="X"
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conceptual translation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The true right end of clone 27K14 (295125) is at 100 in this sequence. This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX 218J18 is from the library RPCIG constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pPAC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 119945)
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HUMAN DNA sequence from clone 218J18 on chromosome Xpl1.3-11.4
Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CCl.3
Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone 218J18 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requests: clonerequest@sanger.ac.uk
During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neighbouring submissions
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/note="MSTD repeat: matches 1.
9767. 9798
/note="Tigger3(Golem) repeat:
consensus"
                                                             /note="MIR repeat: matches 32. .245 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP6-218J18"
/clone_lib="RPCI-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                           'note="MLT1G repeat:
                                                                                                                                                          'note="MER58A repeat:
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'note="MLT1H repeat:
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                                                                                                                                                                                                                                                       'note="MSTD repeat: matches 220.
                                                                                                                                                                                                                                                                                                                                               note="FLAM_C repeat: matches 2. .143 of consensus"
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/note="L2 repeat: matches 2571. .2683 of consensus" 25901. .26177 /note="LTR16A repeat: matches 92. .450 of consensus" /note="LTR16A repea
                                                                                                                                                    complement(join(30021.
/gene-"NDP"
                                                                                                                                                                                                                                                                                            complement(28998)
/gene="NDP"
                                                                                                                                                                                                                                                          complement(29013.
/evidence=not_experimental
/product="NDP (Norrie Disease
                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/product="NDP (Norrie Disease
complement(28998. .53726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1P repeat: matches 4397. .4940 of consensus." 16519. .16720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12459. 12548
/note="MIXTID repeat: matches 20. .
/note="MIXTID repeat: matches 1.
                                                                    codon_start=1
                                                                                                                                                                                                                    'gene="NDP"
                                                                                                                                                                                                                                                                                                                                                                        /gene="NDP"
                                                                                                                                                                                                                                                                                                                                                                                                   complement(28998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476731 R84741 H85821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER33 repeat:
23269. .23575
                                                                                                          note="match: proteins Q00604 P48744"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="FLAM_A repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MC4 repeat: matches 7788. .7954 of consensus":
0579. .20700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="L1M4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="L1P repeat: matches 4891.
7144. .17247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MER74A repeat: matches 1.
15386..16018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLT1D repeat: matches 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match: cDNAs x65724 x65882 x92397; match: I
a045724 AA670439 W61129 N59262 AA045724 AI129296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="8 copies 5 mer tttgt 85% conserved"
4961. .24998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 130. .238 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluSg repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1MC4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="L2 repeat: matches 2410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6904. .16998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="AluSg/x repeat: matches 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="L1MB4 repeat: matches 5181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="L2 repeat: matches 2605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="19 copies 2 mer
5000. .25119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MIR repeat: matches 138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MIR repeat: matches 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .17883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .24096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .18239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .16516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .14210
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                                                                                                                                                                                                                                                          .29019)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       matches 7694.
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                                                                                                                                                                                      .30248,38694.
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(Pseudoglioma))"
                                                                                                                                                                                                                                                                                                                                                                                                                                     (Pseudoglioma))"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .130 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .247 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2522 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .281 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .133 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4985 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2592 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .314 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .324 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .431 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of consensus"
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ACCESSION
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AC022184
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                                                                                                       Homo sapiens chromosome 4 clo
SEQUENCE, 12 unordered pieces
ACO22184
                                                                        AC022184.3 GI:10047716
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                                      HTGS_PHASE1; HTGS_DRAFT
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/note="MIR_repeat: matches 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="LlP4 repeat: matches 5408.
42540. .43017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="31 copies 2 mer ag 90% conserved" 56812. .57069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 2589. .2709 of 53680. .53741
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45355. .45652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 20.
41308. .41535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40405.
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/note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="16 copies 2 mer ac complement(33360. .33924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER5B repeat: matches 58. .178 of consensus"
30652. .30703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30396.
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/db_xref="GI:3947697"
/translation="MRKHVLAASFSMLSLLVIMGDTDSKTDSSFIMDSDPRRCMRHHY
VDS1SHPLYKCSSKMVLLARCEGHCSQASRSEPLVSFSTVLKQPFRSSCHCCRPQTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1M4b repeat: matches 154. .237 of consensus"
44932. .45016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: GSS AQ042323"
33571. .33727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: STS AF020217"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="15 copies 2 mer aa 87% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 2646. .2741 of consensus"
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33007. .33238
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32205. .32377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="AluJb repeat: matches 1. .294 of consensus"
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Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                        clone RP11-52G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .146 of consensus"
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Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 188000; agarose-fp
Insert size: 161309; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs
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6778 6877: gap of 100 bp
6878 8136: contig of 1259 bp in length
8137 8236: gap of 100 bp
8237 9996: contig of 1760 bp in length
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20126: gap of 100 bp
27970: contig of 7844 t
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36727: contig of 8657 t
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12552: contig of 2456 t
52: gap of 100 bp
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nes 22; Conserv
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       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1493)
                                                                                                  Homo sapiens, Similar to diacylglycerol homolog, clone IMAGE:3949350, mRNA, part BC006263
BC006263.1 GI:13623318
                                                        Homo sapiens
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36828 50972; contig of 14145 bp in length
50973 51072; gap of 100 bp
51073 68989; contig of 17917 bp in length
68990 69089; gap of 100 bp
69090 91875; contig of 22786 bp in length
91876 91975; gap of 100 bp
91976 129030; contig of 3278 bp in length
129031 129130; gap of 100 bp
129131 129130; gap of 100 bp
129131 129130; gap of 30795 bp in length
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91976. 129030
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28071. .36727
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12653. .20026
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8237. .9996
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31849 c 32034 g
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129131. .162409
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1. .6777
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/db_xref="taxon:9606"
/chromosome="4"
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                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Cercopithecus
African green monkey.
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Karlins,E., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon;C., Vogt,J.L., Walker,M.A.,
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2390,
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Tissue Procurement: DCTD/DTP
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the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
IRAL Plate: 15 Row: 1 Column: 15.
                                                                                                     cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Similar to diacylglycerol O-acyltransferase (mouse) homolog"
(mouse) homolog"
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NLTYRDLYYFLFAPTLCYELWFPRSPRIRKFELLRRILEMLFFTQLQVGLOGDREFY
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RDWWNSESVTYFWQNNNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLV
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                                                   GI:9796483
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synthetic construct
artificial sequence.
1 (bases 1 to 1895)
Lassner, M. and van Eenennaam, A.
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Sequence 32 from Patent WO0116308
AX090339
AX090339.1 GI:13444205
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Submitted (17-FEB-2000) Pathology,
University School of Medicine, Medi
NC 27106, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 Similarity
20; Conserv
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Joyce, C. W., Davis, M.A., Anderson, R.A. and Rudel, L.L.
                                                                                                                                                                                                     Plant sterol acyltransferases Patent: WO 0116308-A 32 08-MAR-2001;
                                                                                                                                                                                             MONSANTO COMPANY (US)
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/protein_id="AAF98557.1"
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ALTEQAGLLLHVANLATILCFPAAVVLLVESITPVGSLLALMVHTILFLKLFSYRDVN
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572 c 534 g 389 t
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RKRFLKRILEMLFFYOLOVGLIQOMAVPTIONSMK PRIDMDYSSII IEBLIKLAVPNH
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                                                                                                                                     /organism="synthetic construct"
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                                                                                             /note="n=unknown"
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                         Length 1895;
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Direct Submission
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/note="ARGP1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1976)

Oelkers, P., Behari, A., Cromley, D., Billheimer, J.T. and Sturley, S.L. Characterization of two human genes encoding acyl coenzyme A:cholesterol acyltransferase-related enzymes

J. Biol. Chem. 273 (41), 26765-26771 (1998)

98434592
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                H.sapiens mRNA for plakophilin
X97675
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Location/Qualifiers
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1712. .1976
a 639 c 616 g 398 t
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LIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MGDRGSSRRRRTGSRPSSHGGGFAAAEEEVRDAAAGPDVGAAG
DAPAFAPNKOGDAGVGSGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNAR
LFLENLIKYGILVDP1QVYSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGAUT
EQAGLLLHYANLATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWC
RRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKR
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/product="ACAT related gene product 1"
/protein_id="AAC63997.1"
/db_xref="GI:3746533"
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/db_xref="taxon:9606"
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Pred. No.
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Plakophilins 2a and 2b: constitutive proteins of dual location
the karyoplasm and the desmosomal plaque
J. Cell Biol. 135 (4), 1009-1025 (1996)
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Location/Qualifiers
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Revised by [3]
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Submitted (29-APR-1996) C. Mertens, German Cancer Research Center,
Cellbiology, Im Neuenheimer Feld 280, Heidelberg, 69120, FRG
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Conservative
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ERSTFTDSQLGAADMEMTLERAVSMLEADHMPPSTLSAAATFLOHECFOKSEARKRVN
OLRGILKLDLKVONEDVORAVCGALENLVEFEDNDINKLEVAFLINGVPRLLOVLKOTR
OLETKKOITDHTVNLRSRNGWPGAVAHACNPSTLGGQGGRITRSGVRDQPDQHGLLWN
LSSNDKLKNLMITEALLTLENIIIPSGWPEGDYRAGAGLLDEDIFYNVTGCLENIMS
SAGADGRKAMRRCDGLLDSLMYVGRGIADVOPDDKATENCVCILHNISGVLEBAELFE
KYSQNIYIQNRNIQTDNNKSIGCFGSRSRKVKEQYQDVPMPEEKSNPKGVEWLMHSIV
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SNPKGVEWLWHSIVIRMYLSLIAKSVRNYTQEASLGALQNLTAGSGPMPTSVAQTVVQ
KESGLQHTRKMLHVGDPSVKKTAISLLRNLSRNLSLQNETAKETLPDLVSIIPDTVPS
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QLRGILKLLQLLKVQNEDVQRAVCGALEMLVFEDNDNKLEVAELMGVPRLLQVLKQTR
DLETKKQITGLLWNLSSADKLKHLMITEALLITLTENIIIFPSGWPEGDYFKANGLLDE
DIFYNVTGCLRNMSSAGADGRKAMRRCDGLIDSLYHYVRGTIADYQPDDKATENCVCI
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RQYQHGSVSDTVFDSIPANPALLTYPRPGTSRSMGNLLEKENYLTAGLTVGQVRPLVP
LQPVTQNRASRSSWHQSSFHSTRTLREAGPSVAVDSSGRRAHLTVGQAAAGGSGNLLT
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GRGGQTVKSLRIQEQVQQTLARKGRSSVGNGNLHRTSSVPEYVYNLHLVENDFVGGRS
PVPKTYDMLKAGTTATYEGRWGRGTAQYSSQKSVEERSLRHPLRRLEISPDSSPERAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVPKTYDMLKAGTTATYEGRWGRGTAQYSSQKSVEERSLRHPLRRLEISPDSSPERAH
YTHSDYQYSQRSQAGHTLHHQESRRAALLVPPRYARSEIVGVSRAGTTSRQRHFDTYH
RQYQHGSVSDTVFDSIPANPALLTYPRPGTSRSWGNLLEKENYLTAGLTVGQVRPLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="plakophilin 2b"
/protein_id="CAA66264.1"
/db_xref="GI:1871540"
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LLYSLWAHTELHHAYKKAQFKKTDFVNSRTAKAYHSLKD"
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LNNIIQNSYQNARDLLNTGGIQKIMAISAGDAYASNKASKAASVLLYSLWAHTELHHA
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/db_xref="taxon:9606"
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                             Score 20;
Pred. No.
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**NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

** This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Menzel,U., Reichwald,K., Schilhabel,M.B., Wen,G., Siebert,R., Schlegelberger,B. and Chromosome 8 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF205589 133075 bp DNA HTG 01-JUN-2000 Homo sapiens chromosome 8 map 8q24.3-qter clone CTA-393G12, WORKING DRAFT SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Sequencing Center Jena.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biotechnology, Beutenb
3 (bases 1 to 133075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-OCT-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polley, A., Baumgart, C., Blechschmidt, K., Dette, M.D., Jahn, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polley, A., Wen, G., Baumgar Menzel, U. and Rosenthal, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Pr. 1 (bases 1 to 133075)
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                                                                                                                                                                                                                                                                                                                                                                     28206
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8 map 8q24.3-qter"
/chone="CTA-393G12"
                                                            1. .133075
                                                                           ocation/Qualifiers
                                                                                                                                                                       108913:
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Rosenthal, A.
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RESULT 13
AC087588/c
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                               Elhaj.C. Escotto,M., Falls,T., Ferragutto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunarathe,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homsi,F., Howard,S., Huber,J., University, M., Johnson,R., Jolivet,S.,
Jackson,L.E., Jacobson,B., Jla,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Liz,Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Morgan,M., Morris,S., Moser,M., Nickerson,E., Nwokenkwo,S.,
Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Slason,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Tansey,J., Taylor,C., Taylor,P., Tamerisa,A., Tamerisa,K.,
Thomas,S., Uganani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burrch, P., Burkett, C., Burrcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Chen, Z., Chowley, I., Christopoulos, C., Cleveland, C.D., Cox, C., Chen, R., Chacko, J., Chacko, J., Chen, R., Chen, R., Chacko, J., Chacke, J., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Chen, R., Chacke, J., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnard, C., Edgard, D., Edwards, C.C., Elbard, C., Edgard, 
                           Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R. Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walliamson, A., Wleczyk, R., Wooden, S., Williamson, A., Wlezzyk, R., Wooden, D., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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| 38778 c 39111 g 27166 t
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clone_end:T7
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114996. .133075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .16996
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Pred. No.
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1.6;
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                                                                                                                                                   Vinson, R.,
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JOURNAL
REFERENCE
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                                                                             FEATURES
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-JAN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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On Feb 17, 2001 this sequence version replaced gi:12831332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is not known and their order in this sequence record is
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Center clone name: RP11-8P13B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-DEC 1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 5, 2000 this sequence version replaced gi:7329377.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bouslavkiy, L., Boukingalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Cooke, P., Collymore, A., Cooke, P., Collymore, A., Cooke, P., Cooke, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC019269 152511 bp DNA HTG 05-SEP-2000 Homo sapiens clone RP11-8P13, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                 Sequencing vector: Plasmid, n/a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 152511)
Assembly program: Phrap; version 0.960731
Consensus quality: 148050 bases at least Q40
Consensus quality: 150303 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2991
Center clone name: 8_P_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                   1.40579710144928Chemistry: Dye-terminator Big
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27449 c 27320 g 40107 t
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/chromosome="12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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BASE COUNT
ORIGIN
Db 131220 CTGCTGGCGCTGATGGGAGA 131201
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                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                        26 CTGCTGGCGCTGATGGGAGA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
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8619 8718: gap of
8719 13037: contig of 4319 bp in length
13038 13137: gap of
13038 13137: gap of
13138 19064: contig of 5927 bp in length
19065 19164: gap of
19065 27544: contig of 8380 bp in length
19165 27544: contig of 8380 bp in length
27545 27644: gap of
27645 36519: contig of 8875 bp in length
36520 36619: gap of
36620 43866: contig of 7247 bp in length
43867 43966: gap of
100 bp
43867 59245: contig of 15279 bp in length
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10161 110260: gap of
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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RESULT 15
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VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 22, 2000 this sequence version replaced gi:7528181. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Hotton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McCarthy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meldrim, J. Meneus, L. Mihova, T. Miranda, C. Mlenga, V. Morrow, J.
Murphy, T. Naylor, J. Norman, C. H. O'Connor, T. O'Donnell, P.
O'Neil, D. Olivar, T. M. Oliver, J. Peterson, K. Pierre, N.
Pisani, C. Pollara, V. Raymond, C. Riley, R. Rogov, P., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Anderson,S., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. Homo sapiens chromosome 2, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                       * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* This record will be updated and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young,G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukbryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                    Center project name: L9452
Center clone name: 650_N_19
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150666 bases at least Q40
Consensus quality: 150637 bases at least Q30
Consensus quality: 150830 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 159794; sum-of-contigs
                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 161694)
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                                                                                                                                                                                                                        Quality coverage: 4.3 Quality coverage: 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
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clone RP11-650N19 map
                          and the accession number will
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Q20 bases;
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sum-of-contigs
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WORKING DRAFT
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/db_xref="taxon:9606"
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3763: gap of 100 bp
41183: contig of 7420 bp 1
1283: gap of 100 bp
49837: contig of 8554 bp 1
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135838: contig of 16818
100 b
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88506: contig of 15424 bp
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5707:
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72982: contig of 12312 bp
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1: /SIDSI/gcgdata/geneseq/geneseqn/NA1980.DAT: *
2: /SIDSI/gcgdata/geneseq/geneseqn/NA1981.DAT: *
3: /SIDSI/gcgdata/geneseq/geneseqn/NA1981.DAT: *
3: /SIDSI/gcgdata/geneseq/geneseqn/NA1983.DAT: *
3: /SIDSI/gcgdata/geneseq/geneseqn/NA1983.DAT: *
5: /SIDSI/gcgdata/geneseq/geneseqn/NA1985.DAT: *
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7: /SIDSI/gcgdata/geneseq/geneseqn/NA1987.DAT: *
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10: /SIDSI/gcgdata/geneseq/geneseqn/NA1999.DAT: *
11: /SIDSI/gcgdata/geneseq/geneseqn/NA1999.DAT: *
12: /SIDSI/gcgdata/geneseq/geneseqn/NA1993.DAT: *
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1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.

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Gapop 60.0 , Gapext 60.0
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336
1 CGCTGCATCTTTTTCTATGC......CCCCNTTGGTTCCCAACCCA 336
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query	Query			7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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_	20	6.0	1521	19	AAV01533	Human acylcoenzyme
2	20	6.0	1895	21	AAA88842	Human acyl CoA:chc
ω	20	6.0	1895	21	AAZ45383	DNA encoding a pr
4	20	6.0	1976	21	AAA76169	Human ACAT Related
ۍ.	16	4.8	144	19	AAV54158	Nucleotide sequenc
ტ	16	4.8	150	22	AAF95166	embB gene probe.
7	16	4.8	300	21	AAA49869	Mycobacterium tube
8	16	4.8	507	20	AAV89118	EST clone BZ288.
9	16	4.8	528	20	AAX91501	Cloned bovine herp
10	16	4.8	559	20	AAX91502	Bovine herpes viru
11	16	4.8	1234	12	AAQ13722	Lycopene cyclase

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45	44	43	42	41	40	39	38	37	36	<b>3</b> 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	16	16	16	16	16	16	16	16	16	16	16	16
4.5	4.5	4.5		4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8
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.128	1128	1126	1122	120	1117	102	978	858	711	673	513	495	495	488	487	477	459	447	388	274	21	11122	1095	894	737	3056	773	2536	235	1235	1235	1235	.234
21	21	21	21	19	21	21	21	21	21	. 21	16	21	21	21	21	21	21	21	21	21	22	22	19	21	17	21	20	21	18	18	17	17	12
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AAA73738	AAA49032	AAZ97097	AAC34669	AAV05149	AAC50473	AAA96223	AAC41725	AAC59981	AAA65990	AAF15181	AAT26145	AAA35104	AAF21226	AAA16466	AAC36861	AAC51731	AAF08947	AAA67559	AAA67571	AAC05618	AAF96549	AAF25342	AAV58938	AAA39169	AAT12235	AAC77211	AAZ22704	AAA47422	AAT91548	AAT91547	AAT40796	AAT40795	AAQ1372
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Human c	Human (	Human s	Arabidopsis thalia	Nucleotide sequenc	Arabidopsis thalia	cDNA encoding a ma	Arabidopsis	Human secreted pro	E. coli proliferat	Trichoderma reesei	Human gene signatu	Human a	Human ]	Human colon cancer	Arabidopsis	Zea mays	Fusarium venenatum	Eucalyptus grandis	Eucalyptus grandis	Human secreted pro	Human ç	Nucleotide	Mycobacterium tube	Erwinia carotovora	pp60PIK cDNA. Mus	Human ORFX ORF2766	Pseudomonas fluore	Sequence encoding	Genetically engine	Erwinia	Recombinant	Lycopene	Lycopene
cardiac	cardiac	secreted	si sdc	ide	psis	)cod i	psis	ecre	pro	derma	jene	adenosine re	low adenosin	io1or	ps is	S DN	IM VE	tus	tus	ecre	gene		teri	car	CD	DRFX	nonas	e er	ally	her	nant		
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## ALIGNMENTS

DR DR	YP?	Y P A	PR	PF AA	₹ B \$	PN	Υ×	ΕŢ	Ŧ	X S	××	X :	X X	×	E	×	×	AC	×	T 3	RESULT
WPI; 1998-032573/03. P-PSDB; AAW43406.	Sturley SL;	(UYCO ) UNIV COLUMBIA NEW YORK.	30-MAY-1996; 96US-0657620.	30-MAY-1997; 97WO-US09460.	04-DEC-1997.	W09745439-A1.	/*tag= a	CDS 11224	Key Location/Qualifiers	Homo sapiens.	,	therosclerosis: hyperlipidaemi	Acylcoenzyme A:cholesterol acyltransferase II; ARGP-1; ACAT related gene product 1: human: sterol esterification:		Human acvlcoenzyme A:cholesterol acvltransferase II DNA.	U8-JUN-1998 (Ilrst entry)		AAV01533;		AAVO1533 standard: DNA: 1591 RD	RESULT 1

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RESULT
AAA88842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
Genetically engineering the biosynthetic pathways in plants involved the accumulation of sterol compounds and tocopherol to produce compounds for lowering the level of low density lipoprotein cholester in blood serum -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acyl CoA:cholesterol acyltransferase; ACAT; transgenic plant; sterol; tocopherol; phytosterol; phytostanol; anticholesterolemic; hypolipemic; human; ss.
                                                                                                            WPI; 2000-665136/64.
                                                                                                                                                                                                                                                                                                                                                          19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                      WO200061771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human acyl CoA:cholesterol acyltransferase DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA88842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA88842 standard; DNA; 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was identified following database searching for human ACAT-related sequences and use of PCR and RACE to obtain full-length sequences. An isolated nucleic acid (see ANV1534) for human ARGP-2 (see ANW3407) was also identified. Also claimed are host vector systems for production of ARGP polypeptides, and transgenic non-human mammals. ARGP-1 and ARGP-2 nucleic acids can be used to diagnose or treat a subject who has an imbalance in sterol levels due to a defect in sterol esterification. A claimed oligonucleotide capable of sterification. A claimed oligonucleotide capable of sterification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This isolated nucleic acid molecule encodes human acylcoenzyme A:cholesterol acyltransferase II (see AAW43406), or ACAT related gene product 1 (ARGP-1), that is expressed at high levels in intestine and is a candidate for sterol esterification in these tissues. It was identified following database searching for human ACAT-related sequences and use of PCR and RACE to obtain full-length sequences.
                                                                                                                                                                          Venkatramesh M,
                                                                                                                                                                                                                        (MONS ) MONSANTO CO
                                                                                                                                                                                                                                                                                                            12-APR-2000; 2000WO-US09696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1521 BP;
                                                                                                                                                                                                                                                                    12-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding acylcoenzyme A: cholesterol acyltransferase III - useful to identify inhibitors for treatment of atherosclerosis or hyperlipidaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specifically hybridising to a unique sequence of nucleotides in the isolated nucleic acid molecule, or a vector expressing the oligonucleotide, can be used to inhibit wild-type ARGP-1 or ARGP-2. The wild-type enzymes can be used to identify an inhibitor, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Fig 15A-B; 121pp; English.
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20; Conser
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                                                                                                                                                      м, Córbin DR,
Lardizabal KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                  9908-0128995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; Pred. No.
                                                                                                                                                   Bhat GB, B
Lassner MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                 Boddupalli SS,
W, Rangwala SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                      Grebenok RJ;
                                                                                                                                                 Karunanandaa B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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The present sequence encodes a protein related to acyl-CoA:cholesterol acyltransferase (ACAT) related proteins. ACAT-like proteins are active in the formation of a sterol, ester and/or triacylglycerol from a fatt:

fatty

Claim 10; Fig 7; 89pp; English.

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Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                         Novel polynucleotides used for modifying plant oil composition and for developing products for treating e.g. cancer, diabetes, cardiopulmonar; disease or metabolic disorders
                                                                                                                                                                                                                                                      05-JUN-1998;
12-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Acyl-CoA:cholesterol acyltransferase; ACAT; ACAT-like protein; sterol; ester; triacylglycerol; fatty acyl-CoA; lipid composition; plant cell; diacylglycerol acyltransferase; DACAT; triglyceride; cancer; diabetes; cardiopulmonary disease; heart fallure; atherosclerosis; adipocytosis; leukaemia; skin carcinoma; fibroblastoma; metabolic disorder; obesity; abnormal lipid metabolism; abnormal fat absorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sterol brassicastanol. Oil obtained from the seeds can be used in food and pharmaceutical compositions to lower levels of low density lipoprotein cholesterol in blood serum. ACAT enzymes can be used in the present invention to produce elevated levels of phytosterol and/or phytostanol esters.
                                                                                                                                                                                                                                                                                                      04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of human acyl CoA:cholesterol acyltransferases (ACAT) full-length DNA. Sterol O-acyltransferases such as ACAT catalyse the formation of cholesterol esters from cholesterol and long chain fatty acids. Recombinant constructs of the invention are used to alter the biosynthesis and accumulation of sterols and tocopherols in transgenic plants. Seeds of such
                                                                                                                                                                                                                        (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                      09-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ45383 standard; DNA; 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of sterols and tocopherols in transgenic plants. Seeds of such plants may contain elevated levels of sitostanol and/or its esters,
                                                                                                                                                                                                                                                                                                                                                                    WO9963096-A2
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding a protein related to ACAT-like proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1895 BP; 323 A; 610 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and alpha-tocopherol, and reduced levels of campesterol and campestanol and their esters. The seeds may also contain the novel
                                                                                                                                                                                                                                                                                                                                                                                                                                lipoprotein secretion; adipogenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 60-62; 166pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 CTCCCTGCTGGCGCTGATGG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                         2000-105701/09.
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                                                                                                                                                                                        ΨW,
                                                                                                                                                                                       Ruezinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                      98US-0088143
98US-0108389
                                                                                                                                                                                                                                                                                                     99WO-US12541.
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                                                                                                                                                                                        DM;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                       cardiopulmonary
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AAA76169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC activity, including cancer, diabetes, cardiopulmonary diseases e.g. heart CC activity, and sociated with altered cellular disposes, cardiopulmonary diseases associated with abnormal lipid metabolic disorders, obesity, diseases associated with abnormal lipid metabolics, and diseases associated with abnormal lipid metabolics, and diseases associated with abnormal lipid metabolics, and diseases associated with abnormal fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                  New nucleic acid encoding a human diacylglycerol acyltransferase, useful for treating hyperlipidemia, atherosclerosis, heart disease, other diseases associated with an imbalance of triglyceride levels
Claim 4; Fig 1B; 32pp; English.
                                                                                                                                                                                                                                                       01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                          US6100077-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
DGAT; cholesterol; triglyceride biosynthesis; hypertriglyceridaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ACAT Related Gene Product 1 ARGP1 coding sequence
                                                                                                                     P-PSDB; AAB15200
                                                                                                                                                                            Sturley SL,
                                                                                                                                                                                                                                                                                             01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                    08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1895 BP; 323 A; 610 C;
                                                                                                                                                                                                              (UYCO ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         absorption,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524
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                                                                                                                                       2000-557622/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAT Related Gene Product 1; ARGP1; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipoprotein secretion and adipogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                            Oelkers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                  COLUMBIA NEW YORK
                                                                                                                                                                                                                                                         98US-0165042.
                                                                                                                                                                                                                                                                                             98US-0165042
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 245..1711
                                                                                                                                                                                                                                                                                                                                                                                                               /product - "Human ARGP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 1976 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   555 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В 21;
.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme;
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                                                        or.
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The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1) mediates

Query Match

4.88;

Score 16;

DB 19;

Length 144;

Sequence 144

BP;

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23 T; 0

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homeostasis. The present sequence is the coding sequence of human ACAT Related Gene Product 1 (ARGP1). The enzyme encoded by the present sequence is a diacylglycerol acyltransferase (DGAT). ARGP1 does not esterify cholesterol. It is thought therefore that ARGP1 participates in the Coenzyme A-dependent acylation of substrate(s) other than cholesterol e.g. diacylglycerol. Also, ARGP1 has a predicted diacylglycerol binding motif, suggesting that it may perform the last acylation in triglyceride biosynthesis. ARGP1 gene and protein are useful for treating a subject who has an imbalance in triglyceride levels due to a defect in esterification of diglycerol, via gene therapy. Particularly, ARGP1 is useful for treating hypertriglyceridaemia, hyperlipidaemia, atheroselerosis, heart disease, obesity or other diseases associated with habby a contraction of the contraction of diglaceridaemia.
                                            This is the nucleotide sequence of a nucleic acid of the human cell line SH-SY5Y, used in the method of the invention involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related
                                                                                                                                                            Claim 1; Page 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; SH-SY5Y; apoptosis; antibody; immunohistological staining; inhibition; ds.
                              diseases
                                                                                                                                                                                           Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or treating diseases associated with apoptosis
                                                                                                                                                                                                                                              WPI; 1998-495844/42
                                                                                                                                                                                                                                                                                                                                              05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                               05-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                W09839437-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence 3 from human cell line SH-SY5Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV54158 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1976 BP;
                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               high or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sterol esterification, an important component of intracellular lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   excessive levels of triglyceride.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                              97JP-0050302.
                                                                                                                                                                                                                                                                                                                                                                               98WO-JP00905
                                                                                                                                                            70pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 A; 639 C; 616 G; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
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0.12;
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The present invention relates to oligonucleotides based on nucleotide CC Sequences obtained from both wild-type tubercle bacilli (wtTB) that are CC susceptible to a drug and mutant-type tubercle bacilli (mtTB) that are CC resistant to a drug. The drugs used in the present invention are CC rifampicin (RFP), streptomycin (SM), Kanamycin (KM), isoniazid (INH) and CC resistance to INH; the prob gene is responsible for resistance to RFP; the CC resistance to INH; the katG gene is responsible for resistance to INH; the waste gene is responsible for resistance to INH; the waste gene is responsible for resistance to INH; the control of the control of the control of the sequence of tubercle bacilli (TB) responsible for resistance and cc primers used to generate the probes. The present sequence is tubercle bacilli (TB) responsible for resistance and cc present invention can be used to enable the differentiation of drug cresistance and the determination of infection with tubercle bacilli
                                                  Query Match 4.8
Best Local Similarity 100
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                            Sequence 150 BP;
       125
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                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 64; 114pp; English.
             25 CCTGCTGGCGCTGATG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                New oligonucleotides, nucleic acid probes and primers are useful for differentiating drug-resistance and determining infection with tubercle bacilli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-246696/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NISN ) NISSHINBO IND INC. (SYST-) SYSTEM RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-2000; 2000EP-0306563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tubercle bacillus; drug sensitivity; drug resistance; rifampicin; streptomycin; kanamycin; isoniazid; ethambutol; rpoB gene; rrs ge rpsL gene; inhA gene; katG gene; embB gene; probe; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2001 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embB gene probe
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cctgctggcgctgatg
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                                                                                                                            26
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                                                                                                                    A; 50 C; 43
                                                                100.0%;
                                                                                  4.8%;
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                                              Score 16; DB;
; Pred. No. 21;
0; Mismatches
                                                                                                                      G;
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                                                                                                                31 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                             DB 22; Length 150; 21;
                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe; PCR primer; ss.
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В Š

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217 cctgctggcgctgatg

CCTGCTGGCGCTGATG 40

Matches Query Match Best Local

Local

l Similarity 16; Conserv

4.8%; 100.0%;

Score 16; DB; Pred. No. 21; 0; Mismatches

DB 21; 21;

Length 300; Indels

0,

0;

Gaps

0,

G; 63 T;

0 other;

Conservative

0;

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CC The present sequence is that of the Mycobacterium tuberculosis CC ambB (ethambutol resistance) gene (bp7741-8040). Amplification CC and cycle sequencing primers (see AAA4963-62) are used for the CC detection and analysis of antibiotic resistance-associated mutations CC pr (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), l65/rrs. CC (streptomycin) embB (ethambutol), prest, s12 (streptomycin), l65/rrs. CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. CC Characterization of M. tuberculosis present in a sputum sample. CC without prior amplification, to detect the presence of M. CC Cuberculosis, and if present to evaluate the procedure, with or CC tuberculosis, and if present to evaluate the procedure is tuberculosis is detected, a second sequencing procedure is CC performed on the sample to evaluate additional genes for the presence of antibiotic-inducing mutations. CC presence of antibiotic resistance-inducing mutations. Genotypic CC entibiotic treatment options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD
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ID AAA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
      Sequence
                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 8; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                        Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-431611/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis embB gene (ethambutol resistance).
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      300
   B₽;
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44 A; 101 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0111794.
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complement(21..41)
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/note= "primer of AAA49847"
280..300
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92
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RESULT

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AAX91501
ID AAX:
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ID AAV8
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                                                                                               RESULT
                                                                                                                                                                                              Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                       The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, activin/inhibin activity, cathiring activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
              28-SEP-1999
                                                                                                                                                                                                                                                                  Sequence 507 BP; 122 A; 105 C; 101 G; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 116; 618pp; English.
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                                                                     AAX91501 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-1999
                                                                                                                                        173
                                                                                                                                                                  166 AGAATAGTGGGAGTCT 181
                                                                                               ø
                                                                                                                                     therapy; ss.
                                                                                                                                                                                              16; Conser
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Spaulding
                                                                                                                                                                                              Conservative
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                     DNA; 528
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                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                           4.8%; Score 16; DB
100.0%; Pred. No. 22;
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                                                                     ΒP
                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                       Length 507;
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RESULT 10
AAX91502
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprise at least one cytokine-encoding DNA sequence. The expression of cytokines in mammals can up-regulate immune responses to the immunegens. The cytokine is selected from interleukins (IL), colony stimulating factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The BHY-2 based vector or recombinant virus can be used as vaccines. They can be used for preventing or treating a mucosal disease in a subject, e.g. ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly mastitis in cows or breast cancers in humans. They can also be used for preventing or treating a stress-induced disease. The present sequence represents a BHY-2 thymidine kinase partial gene sequence, BHY-2UK cloned for use in the invention. This differs from the previously published sequence BHY-2NT by having adenine at position 727 (full length)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;
tumour necrosis factor; recombinant virus; vaccine; mucosal disease;
mastitis; breast cancer; stress-induced disease; thymidine kinase; ss
                                                                                                                   mastitis; breast cancer; stress-induced disease; thymidine kinase;
                                                                                                                                                tumour necrosis factor; recombinant virus; vaccine; mucosal
                                                                                                                                                                                                                                                                    Bovine herpes virus 2 thymidine kinase partial gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX91502 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 528 BP; 114 A; 176 C; 151 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides bovine herpes virus-2 (BHV-2) based vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY29085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloned bovine herpes virus 2 thymidine kinase partial gene sequence
                                                                                                                                                                                                    Bovine herpes virus-2; BHV-2;
                                                                                                                                                                                                                                                                                                                                    28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bovine
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                                                                                                                                                                             interleukin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        instead of guanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 CCCTGCTGGCGCTGAT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-255101/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Fig 4A-C; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          herpes virus-2 vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                          colony stimulating factor;
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duffas WPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97GB-0020633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 T; 0 other;
                                                                                                                                                                                CSF;
                                                                                                                                                                          CSF; interferon; IFN; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response; immunogen; IL;
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                                                                                                                                                disease;
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Bovine herpesvirus

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Best Local Similarity
Matches 16; Conserv
03-AUG-1990;
02-MAR-1990;
18-MAY-1990;
                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                               04-AUG-1991;
                                                                                                                                                                      05-SEP-1991.
                                                                                                                                                                                                                           W09113078-A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPP; carotenoid; phytoene; zeaxanthin; lycopene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopene cyclase - native.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ13722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ13722 standard; DNA; 1234 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprise at least one cytokine-encoding DNA sequence. The expression of cytokines in mammals can up-regulate immune responses to the immunogens. The cytokine is selected from interleukins (IL), colony stimulating factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The BHV-2 based vector or recombinant virus can be used as vaccines. They can be used for preventing or treating a mucosal disease in a subject, e.g. ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly mastitis in cows or breast cancers in humans. They can also be used for preventing or treating a stress-induced disease. The present sequence represents the partial sequence of a previously published BHV-2 thymidine kinase, BHV-2NY-1. The cloned BHV-2VK sequence (AAX91501) of the invention differs from the present sequence BHV-2NY-1 by having adenine at position 727 (full length) instead of guanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 559 BP; 123 A; 178 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides bovine herpes virus-2 (BHV-2) based vectors that comprise at least one cytokine-encoding DNA sequence. The expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bovine herpes virus-2 vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 CCCTGCTGGCGCTGAT 39
                                                                                                                                                                                                                                                                                                                                                                                                                            herbicola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
90US-0562674.
90WO-4807613.
90US-0525551.
                                                                                                               91WO-US01458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97GB-0020633
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                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                    /*tag= a
/label= lycopene_cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                   EHO-10 (E. vulneris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                      ATCC 39368).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
                                           03-AUG-1990;
02-MAR-1990;
18-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through zeaxanthin diglucoside, which is the final prod. identified in the carotenoid pathway contd. in plasmid pARC376 (contg. a ca. 13 kb chromosomal DNA fragment isolated by Perry et al., J. Bacterio 168:607 (1986). The genes for geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene cyclase, beta-carotene hydroxylase, and zeaxanthin glycosylase are represented in AAQ13716, AAQ13718, AAQ13719, AAQ13722, AAQ13724 and This native communications.
Ausich RL, Brinkhaus FL,
                                                                                          04-AUG-1991;
                                                                                                                                                                                     CDS
                       (STAD ) AMOCO CORP.
                                                                                                                 05-SEP-1991
                                                                                                                                        WO9113078-A.
                                                                                                                                                                                                                        Erwinia
                                                                                                                                                                                                                                           GGPP; carotenoid; phytoene; zeaxanthin; lycopene; ss
                                                                                                                                                                                                                                                                                           26-NOV-1991
                                                                                                                                                                                                                                                                  Lycopene cyclase
                                                                                                                                                                                                                                                                                                                                        AAQ13723 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This native sequence was genetically engineered for use expression in yeast, see AAQ13723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1234 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant expression plasmids can be used of the enzymes and hence large amts. of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are a total of six relevant genes in a 7900 bp region that cause E. coli cells to produce GGPP and the carotenoids phytoene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biosynthesis of carotenoid(s) in genetically engineered using DNA encoding enzymes from Erwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 19(1-3); 313pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ausich RL,
Yen HC;
                                                                                                                                                                                                                                                                                                                                                                                               896 totatcagetcacecg
                                                                                                                                                                                                                                                                                                                                                                                                                      125 TCTATCAGCTCACCCG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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16; Conserv
                                                                                                                                                                                                                     herbicola EHO-10 (E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                           90US-0562674.
90WO-4807613.
90US-0525551.
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    variant

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100.0%;
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Mukharji I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mukharji I,
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Pred. No.
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Proffitt JH,
                                                                                                                                                                                                                      ATCC 39368)
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to produce large amts. carotenoids which they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1234;
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Yarger JG;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are a total of six relevant genes in a 7900 bp region that cause E. coll cells to produce GGPP and the carotenoids phytoene through zeaxanthin diglucoside, which is the final prod. identified in the carotenoid pathway contd. in plasmid pARC376 (contg. a ca. 13 kb chromosomal DNA fragment isolated by Perry et al., J. Bacteriol., 168:607 (1986). The genes for geranyl-peranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene cyclase, beta-carotene hydroxylase, and zeaxanthin glycosylase are represented in AAQ13716, AAQ13718, AAQ13719, AAQ13722, AAQ13724 and AAQ13726 respectively.

The native sequence (AAQ13722) was genetically engineered for use in expression in yeast. At the 5' end of the gene, the native amino acid residue, Arg, was originally encoded by an AGG codon thas been changed to a AGG codon, while retaining its coding for the AGG amino acid residue. Arg, was originally encoded by an AGG codon that was changed to a CGC codon, while retaining its coding for the AGG manno acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
30-OCT-1991;
02-MAR-1990;
18-MAY-1990;
                                                                                                                                                                                                                                          pigment;
tobacco r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosynthesis of carotenoid(s) in genetically engineered hosts using DNA encoding enzymes from Erwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant expression plasmids can be used of the enzymes and hence large amts. of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yen
                                                                                                              US5530188-A
                                                                                                                                                                                                              Erwinia herbicola
                                                                                                                                                                                                                                                                                 GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene;
                                                                                                                                                                                                                                                                                                              Lycopene cyclase
                                                                                                                                                                                                                                                                                                                                          11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                 AAT40795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1234
                                                        02-MAR-1990;
                                                                                  25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      896 tctatcagctcacccg 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 TCTATCAGCTCACCCG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1991-281410/38
                                                                                                                                                                                                                                         ribulose
                                                                                                                                                                                                                                       dehydrogenase-4H; carotenoid; C40; zeaxanthin; diglucoside;
food colourant; chloroplast transit peptide; increase yield;
ribulose bis-phosphate carboxylase-oxygenase; ss.
                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 19(1-3);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
91US-0785566.
90US-0487613.
90US-0525551.
                                                      90US-0487613
                                                                                                                                                   /*tag=
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                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                              coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405
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22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to produce large amts. carotenoids which they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol.,
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PRODUCTION OF THE PRODUCT OF THE PRO
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AAT40796
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Best Local 9
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28-FEB-1991;
21-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manipulation of the present sequence, the lycopene cyclase coding sequence, by in frame linkage to the chloroplast transit peptide (AAW01124) of the tobacco ribulose bis-phosphate carboxylase-oxygenase gene can lead to increased production of total carotenoids in the chloroplast of transformed plants as compared to native, non-transformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and is also in the pathway for biological synthesis of further C40 carotenoids such as zeaxanthin and zeaxanthin diglucoside. Other enzymes involved in the carotenoid biosynthesis pathway include geranylgeranyl pyrophosphate (AAW01113), phytoene synthase (W01121) and phytoene dehydrogenase-4H (AAW01123).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increasing prodm. of total carotenoid(s) in a higher plant - transforming with vector encoding chloroplast transit peptid operably linked to the Erwinia herbicola lycopene cyclase st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ausich
Yarger
                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene; phytoene dehydrogenase-4H; carotene(40); zeaxanthin; diglucosid pigment; food colourant; chloroplast transit peptide; increase yie tobacco ribulose bis-phosphate carboxylase-oxygenase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT40796 standard; DNA; 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 17; Column
                                                                                                                                                                                                                                                                                                                                                                                       Erwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 TCTATCAGCTCACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          897 tctatcagctcacccg 912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lycopene cyclase coding sequence
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91US-0662921.
93US-0095726.
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/product=
18..1165
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                               "SphI-BamHI fragment;
                                                                                                                                                                                                                                               lycopene_cyclase
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
22;
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cyclase structural
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02-MAR-1990;

90US-0487613

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RESULT 15
AAT91547
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28-FEB-1991;
21-JUL-1993;
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02-MAR-1990;
18-MAY-1990;
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Yarger J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a recombinant lycopene cyclase coding sequence. The approx. 1142 bp SphI-BamHI fragment present in the plasmid pARC1509 (ATCC 40850) is used to transform plants in order to increase the level of carotenoids produced by plants. Manipulation of it by in frame linkage to the chloroplast transit peptide (AAW01124) of the tobacco ribulose bis-phosphate carboxylase-oxygenase gene can lead to increased production of total carotenoids in the chloroplast of transformed plants as compared to native, non-transformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and the colou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing prodn. of total carotenoid(s) in a higher plant - by transforming with vector encoding chloroplast transit peptide operably linked to the Erwinia herbicola lycopene cyclase structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is also in the pathway for biological synthesis of further C40 carotenoids such as zeaxanthin and zeaxanthin diglucoside. Other enzymes involved in the carotenoid biosynthesis pathway include geranylegranyl pyrophosphate (AAW01119), phytoene synthase (WO1121) and phytoene dehydrogenase-4H (AAW01123).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 17; Fig 19; 99pp; English.
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                                                                                                                                                                                                                                                      Geranylgeranyl pyrophosphate synthase; Erwinia herbicola; GGPP; lycopene cyclase; recombinant enzyme; transgenic organism;
                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                    AAT91547;
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  US5656472-A.
                                                                                                                                                                                                                                                                                                                          Erwinia herbicola lycopene cyclase structural gene
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                                                                                                                                                                                                                                  beta-carotene; yeast;
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nes 16; Conserv
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91US-0662921.
93US-0095726.
                                                                                                                Location/Qualifiers 20..1144
                                              /product= Lycopene_cyclase
/transl_except= (pos:20..22,aa:Met)
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Search completed: August 24, 2001, 04:36:49 Job time: 2584 sec

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03-AUG-1990;
28-FEB-1991;
07-JUN-1995;
                                                                                                                               A novel DNA molecule has been isolated which encodes an Erwinia herbicola lycopene cyclase enzyme that converts lycopene to beta-carotene The DNA molecule comprises at least 1125 bp and is present in the plasmids pARC147, pARC1509, pARC1510 and pARC1520. The present sequence represents the structural gene for lycopene cyclase. The new DNA molecule can be used to produce the recombinant enzyme and transgenic organisms, e.g. yearsts or plants, with increased beta-carotene levels. Beta-carotene is used as a colourant in margarine and butter and as an intermediate for vitamin A, and may prevent cancer.
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02-MAR-1990;
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                                                                                                                                                                                                                                                                                              DNA encoding Erwinia herbicola lycopene cyclase – for producing recombinant-enzyme, and transgenic organisms with increased
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P-PSDB; AAW32474.
                                                                                                                                                                                                                                                                                                                                                                          Yarger
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                                                                                                         Sequence 1235 BP; 202 A; 384 C; 405 G;
                                                                                                                                                                                                                                                            Example 17; Fig 19; 102pp; English.
                                                                                                                                                                                                                                                                                     beta-carotene levels
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                      125 TCTATCAGCTCACCCG
897 tctatcagctcacccg 912
                                            l Similarity
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                                               Conservative
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1106.813 Million cell updates/sec
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US-08-096-623A-13
US-08-096-623A-15
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54.6844-2
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US-08-335-865J-8
US-08-803-972-1
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* ************************************	ESULT 2 S-08-095-726-13 Sequence 13, Application US/08095726 Patent No. 5530188 GENERAL INFORMATION: APPLICANT: AUSICH, Rodney L APPLICANT: Brinkhaus, Friedhelm L APPLICANT: Mukharji, Indrani APPLICANT: Proffitt, John H APPLICANT: Yarger, James G APPLICANT: Yarger, James G APPLICANT: Yen, Huei-Che B TITLE OF INVENTION: Beta-Carotene Bios TITLE OF INVENTION: Genetically Engine NUMBER OF SEQUENCES: 79 CORRESSEE: AMDOCO COrp., Patents and STREET: 200 E Randolph St CTY: Chicago STATE: IL COUNTRY: USA	Query Match 6.0%; Score 20; DB 3; Length 1976; Best Local Similarity 100.0%; Pred. No. 0.018; Matches 20; Conservative 0; Mismatches 0; Indels 0; 22 CTCCCTGCTGGCGCTGATGG 41 1/11/11/11/11/11/11/11/11/11/11/11/11/	SULT 1 -09-165-042-2 Sequence 2, Application US/09165042 APPLICANT: Sturley, Stephen L. APPLICANT: Oelkers, Peter TITLE OF INVENTION: ISOLATION OF A GENE ENCODING TITLE OF INVENTION: ACYLTRANSFERASE FILE REFERENCE: 0575/5631 CURRENT APPLICATION NUMBER: US/09/165,042 CURRENT FILING DATE: 1998-10-01 NUMBER OF SEQ ID NOS: 32 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 1976 TYPE: DNA ORGANISM: Yeast O99-165-042-2	28 15 4.5 3697 1 US-08-903-91-1 Sequence 30 15 4.5 3697 1 US-08-909-984A-1 Sequence 31 15 4.5 3697 1 US-08-909-983-1 Sequence 32 15 4.5 4371 1 US-08-803-973-1 Sequence 33 15 4.5 4371 1 US-08-803-972-1 Sequence 34 1.4 4.2 3795 3 US-08-484-6868-60 Sequence 35 14 4.2 37 4 US-08-483-1608-60 Sequence 36 14 4.2 37 5 PCT-US91-02568-18 Sequence 37 14 4.2 397 4 US-09-060-756-574 Sequence 38 14 4.2 397 1 US-08-086-410-24 39 14 4.2 399 1 US-08-086-410-24 39 14 4.2 399 1 US-08-086-96-396 Sequence 40 14 4.2 359 3 US-08-989-028-3 41 14 4.2 359 3 US-08-784-582-3 42 14 4.2 359 3 US-08-784-582-3 43 14 4.2 359 3 US-08-784-582-3 44 1.4 4.2 359 3 US-08-784-582-3 45 14 4.2 360 1 US-08-086-410-21 Sequence 46 14 4.2 360 1 US-08-086-410-21 Sequence 47 14 4.2 360 1 US-08-086-410-21 Sequence 48 14 4.2 360 1 US-08-086-410-21 Sequence 49 14 4.2 360 1 US-08-086-410-21 Sequence 40 14 4.2 360 1 US-08-086-410-21 Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com

Floppy disk

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
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                             FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                           PRIOR APPLICATION DATA:
                                                                                                                             SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,72
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yen, Huei-Che B
TITLE OF INVENTION: Beta-Ca
TITLE OF INVENTION: Genetic
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LENGTH: 1235 base pairs
TYPE: nucleic acid
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                                                                                                FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                               APPLICATION NUMBER: US 07/785,566
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                 60680-0703
                                                                                                                                                                                                                                                                                                   Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08095726
                                                                                                                                                                                                                                                                                                                  E: Amoco Corp., Pa
200 E Randolph St
                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Brinkhaus, Friedhelm L
Mukharji, Indrani
Proffitt, John H
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Yarger, James G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ausich, Rodney L
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, NO. 5530188val B
                                                                                                                                                                                                                                                                                                                                                                                  Beta-Carotene Biosynthesis in
Genetically Engineered Hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                 us/08/095,726
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                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096.623A
FILING DATE: 22-TUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                                                              APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/525,551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: APPLICANT:
REFERENCE/DOCKET NUMBER: AM TELECOMMUNICATION INFORMATION:
                                                                                                                              FILING DATE: 18-MAY-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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APPLICANT: Yen, Huei-Che B.
TITLE OF INVENTION: Blosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
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                                                                    FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
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                                    REGISTRATION NUMBER: 29,381
                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                     Gamson, Edward P
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120 S. Riverside Plaza, 22nd Floor
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3128564972
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                                                                                                              US 07/487,613
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                     AMO-006.1
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Best Local Similarity
                                                                                               PRIOR APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/562,674
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/525,551
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/805,061
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POSITION IN GENOME:
MAP POSITION: -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: BITITLE OF INVENTION: GINUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                             APPLICATION NUMBER: US 07/487,613 FILING DATE: 02-MAR-1990 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 09-DEC-1991
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 22-JUL-1993
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REFERENCE/DOCKET NUMBER: AMO-006.1
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120 S. Riverside Plaza, 22nd Floor
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Mukharji, Indrani
Proffitt, John H.
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Pred. No.
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US-08-096-623A-15
                                                                           ; NAME/KEY:
; LOCATION:
US-08-259-264-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (312) 655-1501 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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POSITION IN GENOME:
MAP POSITION: -19
UNITS: bp
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 5737 base pairs
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: pp60PIK: A DOWNSTREAM ELEMENT IN INSULIN SIGNALING NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                         FEATURE:
                                                                                                                                        MOLECULE TYPE:
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TYPE: n
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 10-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC
SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                    STRANDEDNESS:
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DEDNESS: single
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N: 435
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                             Length 5737;
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RESULT 7 US-08-822-586-45

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Sequence 45, Appa-
Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08203806B Patent No. 5714575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/437
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7803 CCTGCTGGCGCTGATG 7818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/82
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WIILIAM R. JAC APPLICANT: AMALIO TELENTI
                                                                       TITLE OF INVENTION: Nucleic Acid Sequences, Stress-induced TITLE OF INVENTION: Proteins and Uses Thereof NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 10016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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   ADDRESSEE:
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                                                                                                                                                                              : Jones, Pamela
Etchegaray, Jean-Pierre
Weining, Jian
Pollitt, N. Stephen
Goldstein, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08822586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
Weiser & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO
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US-09-106-217-15

; Sequence 15, Application US/09106217

; Patent No. 6063576
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REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEPHONE: 215-875-8394
TELEX: 834809 WEISTAK
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/203,806B
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION NAME: Saxe, Stephen A.
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS: ADDRESSEE: Rothwell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                      STREET: 555 Thirteenth
STREET: Tower
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity hes 15; Conserv
                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                      COUNTRY: U
ZIP: 20004
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                                                                         APPLICATION NUMBER: US/09/106,217
                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                  Cardiomyopathy, a Heritable Form of Heart Failure
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                            Figg, Erns
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                                                                                                                                                                                                                                                                                                et, N.W., Suite 701 East
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TELECOMMUNICATION INFORMATION:

REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:

38,609

2323-125

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Best Local Similarity
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                                                                                                                                                                          APPLICATION NUMBER: US/09/106,217 EILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE
HYPOTHETICAL: NO
                                                                                                               TELEFAX: 202-783-6031 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-783-6040
                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                     TOPOLOGY:
                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
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STRANDEDNESS: doub
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                                                                                                                                           TELEPHONE:
                                                                                 ENGTH:
                                                                nucleic acid
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                                                                               1134 base pairs
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L00.0%; Pred. No.
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; LOCATION:
US-09-106-217-1
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Best Local Similarity
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,084
FILING DATE: 30-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/690,840
FILING DATE: 23-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/869,293
FILING DATE: 14-APR-1992
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FEATURE:
                                                                                                                           TELEFAX: (415) 576-0300
NFORMATION FOR SEQ ID NO:
                           STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                          REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                          FILING DATE: 14-APR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 GAGGCACCACTATGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 GAGGCACCACTATGT 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
NAME/KEY: CDS
                                                                                            LENGTH:
                                                          nucleic acid
DEDNESS: single
                                                                                                                                                                                                                             Parent, Annette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lerch, Bernard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sharma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                               linear
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; LOCATION: 1..1350
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-462-351-1
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5468481-2
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5468481-2/c
;Patent No. 5468481
; APPLICANT: SHARMA,
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Query Match
Best Local Similarity
....hes 15; Conserve
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5194425-2/c
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Best Local S
Matches 15
                                                                                                                    FILING DATE:
SEQ ID NO:2:
                                                                                                                                                                                                              TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL AMELIORATING AUTOIMMUNITY NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           BRIAN R.
                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L. TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                      PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                        APPLICANT: SHARMA , SOMESH D.; LERCH, L. BERNARD; CLARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 690,840
FILING DATE: 23 APR-1991
APPLICATION NUMBER: 576,084
FILING DATE: 30 AUG-1990
APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792 AGACAGCAAAACGGA 778
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|||||||||||||||||
| 792 AGACAGCAAAACGGA 778
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les 15; Conserv
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FILING DATE: 21-JUN-1989
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 21-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 635,840 FILING DATE: 28-DEC-1998 APPLICATION NUMBER: 367,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                       APPLICATION NUMBER: 210,594 FILING DATE: 23-JUN-1988
                                                                                                        LENGTH: 1356
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                4.5%; Score 15; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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100.0%; Pred. No.
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alpha subunit"
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16;
                                 DB 6;
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US-08-812-203-4
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                                                                                                                                               US-09-300-864-4
                                                                                                                                                            RESULT 15
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                                                                                                             Sequence 4, Application US/09300864 Patent No. 6214972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION W:
REGISTRATION NUMBER: MAL 94/185
REFERENCE/DOCKET NUMBER: MRL 94/185
TELEPHONE: (908)594-3905
                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: (908)594-4720
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                              1145 CTGCTGGCGCTGATG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                 APPLICANT:
                                              APPLICANT:
                                                               APPLICANT:
                                                                                APPLICANT:
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 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: RAHWAY
                                                                                                                                                                                                                                           26 CTGCTGGCGCTGATG 40
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                                                                                                                                                                                                                                                                                                                                                                                                                       : 1488 base pairs
nucleic acid
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METTERS, KATHLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABRAMOVITZ, MARK
                                                                ABRAMOVITZ, MARK BOIE, YVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLIPETZ,
                                                                                                                                                                                                                                                                             Conservative
               SAWYER, NICOLE
METTERS, KATHLEEN
SLIPETZ, DEBORAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-1997
                                                                                                                                                                                                                                                                                            4.5%; Score 15; DB
100.0%; Pred. No. 17;
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DNA ENCODING PROSTAGLANDIN RECEPTOR DP
DNA ENCODING PROSTAGLANDIN RECEPTOR DP
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                                                                                                                                                                                                                                                                               0,
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                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                  Gaps
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NUMBER OF SEQUENCES: 4

CORRESSONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. Box 2000
CITY: RAINAY
COLVETT: 126 E. LINCOLN AVE., P.O. Box 2000
CITY: RAINAY
COUNTRY: USAN
ITH O7055-0900
COMPUTER ELDAN TYPE: FLOPPY disk
COMPUTER: INJ
COUNTRY: USAN
COMPUTER: INJ
COUNTRY: USAN
COUNTRY: USAN
COUNTRY: USAN
COUNTRY: USAN
COUNTRY: USAN
COUNTRY: USAN
COUNTRY: UNUMBER: US/09/300.864
FILING DATE:
CLASSIFICATION UNUMBER: US/09/300.864
FILING DATE:
APPLICATION UNUMBER: US/09/300.864
FILING DATE:
FERENCE, DOCKET NUMBER: MRL 94/185
FELENGHUNE: (908)594-3905
FELENGHUNE: (908)794-300
FELENGHUNE: (908)794-300
FELENGHUNE: (908)79
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em\_esthum20:\*
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em\_esthum24:\*
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em\_esthum26:\*

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                     Takasuga, A., Itoh, R., Jitohzono, A. and
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BF733499 RC6-AN006
AZ015284 RPC1-Z3-Z
AW964683 EST376756
BE337999 601290548
AQ984383 RPC1-Z3-3
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Unpublished (2000)
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukush
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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This clone was obtained from Location/Qualifiers
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This clone was obtained from a Location/Qualifiers
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1 (bases 1 to 539)
Sugimoto, Y., Hirotsune, S.,
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Contact: Yoshikazu Sugimoto
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/dev_stage="fetus"
/lab_host="DH10B"
/note="vector: pZL1; Site_1: Sal1; Sit
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/tissue_type="brain"
/dev_stage="fetus"
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
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AV663492 Bos taurus
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Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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cDNA clone E1BR036H10
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1 (bases 1 to 409)
Sugimoto, Y., Hirotsune, S.,
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Unpublished (2000)
Contact: Yoshikazu Sugimoto
Animal Genetics Division
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AV663813.1
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3', mRNA
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This clone was obtained from a polyA-deleted
Location/Qualifiers
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                     Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COW.
                                                                                                               Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Yoshikazu Sugimoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugimoto, Y., Hirotsune, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
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                                                                                                                                                                                                Email: kazusugi@cocoa.ocn.ne.jp
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/db_xref="taxon:9913"
/clone="ElBR036H10"
/clone="ib="Bos taurus b
/tissue_type="brain"
/dev_stage="fetus"
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/note="Vector: pzL1; Site_1: ',
/note="Vector: pzL1; Site_1: ',
/note="Vector: pzL1; Site_1: Site"
was deleted from a Not1 site"
/note="pz_1" site" si
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E1BR038G07"
                                                                                          1. .414
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BE121364
BE121364.1 GI:8513469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message, cDNA Library Preparation: M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa
451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 435)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two appr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
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                                                                                        /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CAO-bax-a-08-0-UI"
/clone="UI-R-CAO"
/clone="Ib="UI-R-CAO"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT713D-Pac (Pharmacia) with a modified
/note="vector: pT713D-Pac (Pharmacia) with a modified
/note="vector: pt713D-Pac (Pharmacia) with a modified
/note="vector: pt713D-Pac (International For a for the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
, midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus, For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.ulowa.edu. The subtraction has been
                     D
              site at ratest.eng.uiowa.edu. The previously described in (Bonaldo, Genome Research 6:791-806, 1996)
TAG_SEC-None found*
106 c 114 g 115 t
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/tissue_type="brain"
/dev_stage="fetus"
/lab_host="DHIOB"
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Pred. No.
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0.019;
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                                                                              Lennon and Soares,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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UI-R-CAO-bhe-c-02-0-UI.S1 UI-R-CAO Rattus norvegicus
UI-R-CAO-bhe-c-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
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Bonaldo, M.F., Lennon
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106 c 114 g
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/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CA0
library is a subtracted library derived from the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
/ midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest and union add.
                                                                                                                                                                                                                         site at ratest.eng.uiowa.edu. Ti
previously described in (Bonaldo,
Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
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/db_xref="taxon:10116"
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/clone_lib="UI-R-CAO"
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UI-R-CAO-bha-c-12-0-UI.s1 UI-R-CAO Rattus norvegicus
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Program for Rat Gene Discovery and Mapping
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
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451 Eckstein Medical Research Building Iowa City,
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Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 66 row: K column: 23
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Keele, J.W.
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musicae; I to 711)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST discovery in swine
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10371 row: n column: 12
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                                                                                                                         Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies,
                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence
BG293757
                                                                                                                                                                                                                                                                                                                                                                                                                                      BG293757 711 bp mRt
602390647F1 NIH_MGC_94 Mus
                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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178 c 149 g 110 t
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/tissue_type="pooled"
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/db_xref="taxon:9823"
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11 TTTTCTATGCTCTCCCTGCTGG 32
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AU135898
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                         Similarity 100.
22; Conservative
                                                                                                                                                                                                                                    Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                         Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                              Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                        HRI human cDNA project
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 796)
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AU135898.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH108 (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 196 c 150 g 185 t
                                                                                                            /tissue_type="placenta"
/note="Vector: pME18SFL3"
207 c 197 g 180
                                                                                                                                                    /clone="PLACE1003129"
/clone_11b="PLACE1"
                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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PLACE1003129 5', mRNA
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11 TTTTCTATGCTCTCCCTGCTGG 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL541183 900 bp mRNA EST 16-FEB-2001 AL541183 LTI_FL002_PL1 Homo sapiens cDNA clone CSODE005YD14 5 prime
                                        Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                              AL537924 952 bp mRNA EST 13-FEB-2001
AL537924 LTI_FL013_FBrn1 Homo sapiens cDNA clone CSODF028Y018 5
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1 (bases 1 to 900)
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                 prime, mRNA sequence.
AL537924
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Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Genoscope
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/db_xref="taxon:9606"
/clone="CSODE005YD14"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not and cloned into the Not I and Eco R vaites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://fulllength.invitrogen.com"
238 c 213 g 222 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                           GI:12801417
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100.0%;
                                                                                                             Jessee, J. and Polayes, D.
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Pred. No.
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EST26541 Cerebellum
AA323481
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                      Contact: Kerlavage, AR
                                                                                                                                                                              Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                      Venter, J.C.
                                                                                         The Institute for Genomic
                                                                                                                Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 179)
                                            12 Medical Center
1: 3018699056
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Location/Qualifiers
arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and Eco RV sites of the and cloned into the Not I and Eco RV sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
251 c 224 g 245 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses
week, 24 week and 26 week)"
/lab_host="DH10B"
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Eukaryota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
1 (bases 1 to 371)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White, Y., Wylie, T., Watersto
Washu-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Cerebellum II"
/tissue_type="cerebellum"
/dev_stage="adult"
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/db_xref="ATCC (inhost):124262"
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/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)
/lab_host="D
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:5939614"
/db_xref="taxon:9606"
/db_wref="taxon:9606"
/clone="IMAGE:739933"
/clone_11b="Soares ovary tumor NbHOT"
/sex="Female"
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